

588 ---LDTLKLAI-----GTYTEHKSSWEGLMRRRGMGRDYSWENAAIOYE 627

RESULT 14

starch synthase (EC 2.4.1.21) precursor - rice
N;Alternate names: starch synthase
C;Species: *Oryza sativa* (rice)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 16-Aug-2002
C;Accession: JQ2322; PQ0811
R;Baba, T.; Nishihara, M.; Mizuno, K.; Kawasaki, T.; Shimada, H.; Kobayashi, E.; Ohnishi, K.
Plant Physiol. 103, 565-573, 1993
A;Title: Identification, cDNA cloning, and gene expression of soluble starch synthase in rice
A;Reference number: JQ2322; MWID: 94302151; PMID: 7518089
A;Accession: JQ2322
A;Molecule type: mRNA
A;Residues: 1-626 <BAB1>
A;Cross-references: DDBJ: D16202; NID: g450484; PIDN: BAA03739.1; PID: g450485
A;Accession: PQ0811
A;Molecule type: protein
A;Residues: 114-129 <BAB2>
A;Experimental source: seed
C;Function:

RESULT 15

starch synthase (EC 2.4.1.21) isoform STSII-1 - maize (fragment)
T01208
N:Alternate names: starch synthase isoform STSII-1
RESOUR 15

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 13:50:41 ; Search time 8.74119 Seconds
(without alignments)
3088.950 Million cell updates/sec

Title: US-09-980-771A-3_COPY_58_708
Perfect score: 3370
Sequence: 1 ALDIVVAAAEVAPWSKITGL.....SASKTSRAKPLVSRATKSA 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1481.5	44.0	608	1	UGST_MANES
2	1457.5	43.2	607	1	UGST_SOLTU
3	1455.5	43.0	608	1	UGST_ANTWA
4	1415.5	42.0	603	1	UGST_PEA
5	1412.5	41.9	608	1	UGST_IPOBA
6	1397.5	41.5	609	1	UGST_ORYSA
7	1395.5	41.4	603	1	UGST_HORVU
8	1394.5	41.4	609	1	UGST_ORYGL
9	1362	40.4	615	1	UGST_WHEAT
10	1355.5	40.2	608	1	UGST_SORBI
11	1353.5	40.2	605	1	UGST_MAIZE
12	902.5	26.8	641	1	UGS2_SOLTU
13	873.5	25.9	626	1	UGS2_ORYSA
14	871	25.8	752	1	UGS3_PEA
15	869	25.8	610	1	UGS2_WHEAT
16	847.5	25.1	788	1	UGS3_SOLTU
17	684.5	20.3	477	1	GLGA_STRPN
18	677.5	20.1	484	1	GLGA_BAGSU
19	670.5	19.9	485	1	GLGA_BAGST
20	669	19.9	478	1	GLGA_LACLA
21	653.5	19.4	480	1	GLG1_RHIME
22	652	19.3	480	1	GLGA_AGR5
23	651	19.3	486	1	GLGA_THEMEA
24	646.5	19.2	480	1	GLGA_RHTR
25	637	18.9	477	1	GLGA_CLOAB
26	622	18.5	482	1	GLGA_CLOPE
27	622	18.5	484	1	GLGA_VIECH
28	614.5	18.2	476	1	GLGA_BACHD
29	604.5	17.9	486	1	GLG2_RHIME
30	604	17.9	476	1	GLGA_YERPE
31	602.5	17.9	481	1	GLGA_RHILU
32	587	17.4	477	1	GLGA_ECOLI
33	587	17.4	477	1	GLGA_SALTU

34	580	17.2	477	1	GLGA_SALTU
35	578	17.2	480	1	GLGA_PASMU
36	569	16.9	476	1	GLGA_HAFIN
37	568.5	16.9	1230	1	UGS4_SOLTU
38	560.5	16.6	472	1	GLGA_ANASP
39	555	16.5	461	1	GLGA_FUSNN
40	552.5	16.4	463	1	GLGA_AQUAE
41	538	16.0	465	1	GLGA_SYN7
42	536	15.9	477	1	GLGA_RHOSH
43	536	15.9	492	1	GLG2_ANASP
44	535	15.9	477	1	GLGA_SYNY3
45	527	15.6	444	1	GLGA_DEIRA

ALIGNMENTS

RESULT 1
UGST_MANES STANDARD; PRT; 608 AA.
AC Q43784;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
GN WAXY OR GBSS.
OS Manihot esculenta (Cassava) (Manioc).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids I; Malpighiales; Euphorbiaceae; Manihot.
OX NCBI_TaxID=3983;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. M.COL 22; TISSUE=Tuberous root;
RX MEDLINE=94083565; PubMed=8260633;
RA Salehuzzaman S.N., Jacobsen E., Visser R.G.F.;
RT "Isolation and characterization of a cDNA encoding granule-bound
starch synthase in cassava (Manihot esculenta Crantz) and its
antisense expression in potato."
RL Plant Mol. Biol. 23:947-962(1993).
CC -! FUNCTION: RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE IN RESERVE
STARCH.
CC -! CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -! PATHWAY: Starch biosynthesis
CC -! SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -! TISSUE SPECIFICITY: SYNTHESIZED IN A NUMBER OF DIFFERENT ORGANS,
BUT MOST ABUNDANTLY IN TUBERS.
CC -! SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; X74160; CAA52273.1;
InterPro; IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
FT Transit peptide; Chloroplast; Starch biosynthesis.
FT TRANSIT 1 78 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 79 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 608 AA; 66968 MW; C9C970CD3011BDBB CRC64;

Query Match 44.0%; Score 1481.5; DB 1; Length 608;
Best Local Similarity 55.0%; Pred. No. 2.4e-81;
Matches 299; Conservative 64; Mismatches 148; Indels 33; Gaps 9;

RC	STRAIN=cv. Dongnong 303;		
RA	Dai W.L., Deng W., Cui M., Xiu M., Zhao S.Y., Wang X.M.;		
RL	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.		
CC	-!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =		
CC	UDP + {(1,4)-alpha-D-glucosyl}(N+1).		
CC	-!- PATHWAY: Starch biosynthesis.		
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.		
CC	-!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE		
CC	FAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL; X58453; CA441359.1; -		
DR	EMBL; X83220; CA58220.1; -		
DR	PIR; S16555; YUPOY.		
DR	InterPro; IPR001296; Glycos_transf_1.		
DR	Pfam; PF00534; Glycos_transf_1; 1.		
KW	Glycogen biosynthesis; Transferase; Glycosyltransferase;		
KW	Transit peptide; Chloroplast; Starch biosynthesis.		
FT	TRANSIT 1 77 CHLOROPLAST.		
FT	CHAIN 78 607 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.		
FT	BINDING 95 95 UDP-GLUCOSE (BY SIMILARITY).		
FT	CONFLICT 130 130 A -> T (IN REF. 3).		
FT	CONFLICT 398 398 I -> V (IN REF. 3).		
FT	SEQUENCE 607 AA; 66575 MW; 2A377865CFafa650 CRC64;		
QY	Query Match 43.2%; Score 1457.5; DB 1; Length 607;		
Db	Best Local Similarity 54.0%; Pred. No. 6.6e-80;		
Db	Matches 295; Conservative 67; Mismatches 143; Indels 41; Gaps 10;		
QY	2 LDIVMAAEVAPWSKTGGLGVDVGGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 60		
Db	81 MNLIFVGTGTEVGPWSKTGGLGVDVGGGLPPALARGHRVMTISPRYDQYKDAWDTSVAVEVK 140		
QY	61 MG---EKVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRFPALFC 117		
Db	141 VGDSIEIVREFHCYKRGVDRVDFVDPHMFLEKVGKTSKIYGPKAGLDYLDNELRFSLLC 200		
QY	118 KAATEARVLPF-----GP-GEDCVFVANDHWSALVPLVKDEYQKQFTKAKSVLA 169		
Db	201 QAALAEAPKVLNLSNNSYSGPYGEDVLFITANDMHTALIPCYLKSMTQSGIYLNKAVFC 260		
QY	170 IHNIAFOGRWEEAFKDTKLPPAAFDKLAISDGAKVYVTEATPMEDEKPELTKTKYKKI 229		
Db	261 IHNIAFOGRFASDFPRLNLPDKFKSSDFIDGYEK-----PVKG---RKI 303		
QY	230 NWLKGIIAADKLVTVSPNYATEIAADAAGGVDELDTVIRAKGIEGIVNGMDIEWNPKTD 289		
Db	304 NNMKAGILESHRVTVSPYTAQELVSAVDKGVLEDSVLRTKCTITGVNGMDTQEWNPATD 363		
QY	290 KFLSAPYDQNSVYAGKAAKEALQALGELGVPDPTAPLFAFIRGLEEQKGVDIILAALPKI 349		
Db	364 KYTDVKYDITVTMDAKPLLEKALQAAVGLPDKTPIGLTIGIRLEEQKSGDIIAAAHKF 423		
QY	350 LATPKVQIALLGTGKAAYEKLIVNAIGTKYGRAGVGVKFSAPLAHMLTAGADFMVPSRF 409		
Db	424 IGL-DVQIVLVTGKKEFEQIEQLLEVLPNKAAGVAKFNVPPLAHMITAGADFMVPSRF 482		
QY	410 EPCGLIQLHAMHYGTVPVASTGGVLDVTVKESVTFGHMGALNP--DKLDEADADALAATV 467		
Db	483 EPCGLIQLHAMRYGTVPICASTGGLVDIVKESYTFGHMGALNP--DKLDEADADALAATV 542		
QY	468 RRASEVFAAGGRYPPEMVANCIQSODLSWSKPAOKWEGLEEVYKGVGATAKEETKVPVA 519		
Db	543 ARALAVYGTALFAEMIKNCNCSSELSWKEPAKKWETLLILGLCASGSEPGVEGE-EIAPLAK 601		
QY	520 EEIKVP 525		


```

RESULT 6
UGST_ORYSA
ID UGST_ORYSA STANDARD; PRT; 609 AA.
AC P19395; 043013;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
DE WAXY OR WX.
GN WAXY OR WX.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RN SEQUENCE FROM N.A.
RN TISSUE=Seed;
RN MEDLINE=92322986; PubMed=1377969;
RX Okagaki R.J.;
RT "Nucleotide sequence of a long cDNA from the rice waxy gene.";
RL Plant Mol. Biol. 19:513-516(1992).
RN [2]
RN SEQUENCE FROM N.A.
RN STRAIN=cv. Japonica Taichung 65; TISSUE=Seedling;
RX Hirano H.Y., Sano Y.;
RT "Molecular characterization of the waxy locus of rice (Oryza
RT sativa).";
RL Plant Cell Physiol. 32:989-997(1991).
RN [3]
RN SEQUENCE FROM N.A.
RN STRAIN=cv. Japonica, and cv. Hanfeng;
RX MEDLINE=91016948; PubMed=2216792;
RX Wang Z.Y., Wu Z.L., Xing Y.Y., Zheng F.G., Guo X.L., Zhang W.G.,
RX Hong M.M.;
RT "Nucleotide sequence of rice waxy gene.";
RL Nucleic Acids Res. 18:5898-5898(1990).
RN [4]
RN SEQUENCE FROM N.A.
RN STRAIN=cv. Indica;
RX Wang X.O., Wang Z.Y., Hong M.M.;
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE OF 153-343 FROM N.A.
RX MEDLINE=91200672; PubMed=2016064;
RX Shimada H., Tada Y.;
RT "Rapid isolation of a rice waxy sequence: a simple PCR method for the
RT analysis of recombinant plasmids from intact Escherichia coli
RT cells.";
RL Gene 98:243-248(1991).
CC -!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X62134; CAA44065.1; -
CC EMBL; X58228; CAA41186.1; -
CC EMBL; X53694; CAA37732.1; -
CC EMBL; X65183; CAA46294.1; -
CC EMBL; M55039; AAA33918.1; -
CC PIR; JQ0703; JQ0703.
CC PIR; S22519; S22519.

```


Matches	212;	Conservative	90;	Mismatches	161;	Indels	69;	Gaps	19;
QY	3	DIVMAAEEVAPWSKTGGGLDVTGGLPIELVKRHRVMTIAPRY-----DOYADAWDTS	55						
Db	132	NIIFTAAAPYSKTGGGLDVCSGSIIPALAAARHVRVWVSPRYLNGSPSDEKAYANAVDL	191						
QY	56	V--VVDIMG--EKVYRPHSIKKGVHRVMDHPWFLAKVWGSTKSLKPGPSGADYLDNHK	111						
Db	192	VRATVHCFDGAQAEVAFYHEYRAGVDWVFEVHSSYC-----RPETP-YGDIYGA-FG	244						
QY	112	REFALCKAAIEAARVLPFGP--GEDCVFVANDWESALVPLVKDEYOPKQFTKAKSVL	168						
Db	245	RETLSSHAAACEAPLVLPGLGGTYGKCLFLANDWHAALVPLLLAAKTRPGVYVDARSIV	304						
QY	169	AHNIAFOGRWEEAEFKDTKLPOAAFDKLAESDGYAKVYTEATPMEDEKPPITGKTYKK	228						
Db	305	AHNIAHQGVPEAVIYNLGLPPQWYGAV---EWIFFTWARAHALD-----TGET---	351						
QY	229	INWLKGGIITADKLVTVSPNATEIAADAAGVDELDTVI--RAKIGIEVINGMDIEWNP	286						
Db	352	VNVLKGAIVADRIILTVSGYSWEITT--PEGYGIHELLSSRSQVINGITNGIDVNDWP	410						
QY	287	KTDKFLSAPYDONSVYAGKAAKEALQAEGLPVDPTAPLFAFICGLEBQKGVDIILAA	346						
Db	411	STDEHTASHYSINDL-SGKVQCKTDLOKELGPIRPDCPLGFTIGRLDYKQGVDIILSAI	469						
QY	347	PKILATPKVQIAILGTGKAAAYEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADFMVLP	406						
Db	470	PELMQN-DVOVNLMSGEKQYEDWMRHTENLFKDFRAWGVNFVPSHRTAGCDIILMP	528						
QY	407	SRFEPCLGLIQLHAMHYGVVVPVASTGGVLVDIVK-----EGV---TGFHMGALNP	456						
Db	529	SREPCGLNQLYAMRYGTIPVHSTGGRLDTYKDFNPYAQEGIGBGTGWTSPITSEKL-	587						
QY	457	EADADALAAATVRRASEVFAGGRYPE-----MVANCISDLSKSPAKQKE	501						
Db	588	---LDTLKLAI-----GIYTHKSWEGLMRMRGDRYSWENAAIQYE	627						
RESULT 13									
UGS2_ORYSA	STANDARD;	PRT;	626	AA.					
ID	UGS2_ORYSA								
AC	Q40739;								
DT	01-NOV-1997 (Rel. 35, Created)								
DT	01-NOV-1997 (Rel. 35, Last sequence update)								
DT	15-JUN-2002 (Rel. 41, Last annotation update)								
DE	Soluble glycogen [starch] synthase, chloroplast precursor								
DE	(EC 2.4.1.11) (SS).								
OS	Oryza sativa (Rice).								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;								
OC	Erbartoideae; Oryzeae; Oryza.								
OX	NCBI_TaxID=4530;								
RN	[1]								
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 114-131.								
RC	STRAIN=cv. Japonica; TISSUE=Seed;								
RX	MEDLINE=94302151; PubMed=7518089;								
RA	Baba T., Nishihara M., Mizuno K., Kawasaki T., Shimada H.,								
RA	Kobayashi E., Ohnishi S., Tanaka K.-I., Arai Y.;								
RT	"Identification, cDNA cloning, and gene expression of soluble starch								
RT	synthase in rice (Oryza sativa L.) immature seeds.";								
RL	Plant Physiol. 103:565-573(1993).								
CC	-!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =								
CC	UDP + {(1,4)-alpha-D-glucosyl}(N+1).								
CC	-!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE.								
CC	-!- TISSUE SPECIFICITY: LEAVES AND IMMATURE SEEDS.								
CC	-!- MISCELLANEOUS: THREE FORMS OF SOLUBLE STARCH SYNTHASE WERE								
CC	PURIFIED: RSS1, RSS2 AND RSS3.								
CC	-!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE								
CC	FAMILY.								
CC	-----								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration								

300	NMKAGILEADRLTVSPYAEELISGIARGCELDNIMRLTGTITGIVNGMDVSEWDPDSRD	359
290	KFLSAPYDONSYYAKAAKALQAEGLPVPDPTAPLFAFICGLEBQKGVDIILALPKI	349
360	KYIAKVDYSTAVEAKALNKEALQAEVGLPVDNRNPLVAFICGLEBQKGFVWAAIPQL	419
350	L-ATPKVQIAILGTGKAAYEKILVNAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSR	408
420	MEMVEDQVILGTGCKKFERMLMSAEKFPCKVRAVVKFNAALAHHINAGADVIAVTSR	479
409	FEPCLGLIQLHAMHYGTPVWVASTGGVLVDVTKGVTGFHMGALNPD--KLDEADADALAAT	466
480	FEPCLGLIQLQMRGTPPCASTGGVLVDIIEGTFHMGRLSDVCNVVPEADVKKVATT	539
467	VRASEVFAGGRYPENVANCISDLSKSPAKORWGLLEB--VYKGGV-----ATAKK	519
540	LQRAIKVGTGPAYEYVRNMIQDLSWKGPKNWENVLISLVAGGEPGVEGEIAPLAK	599
520	EIKVP 525	
600	ENVAAP 605	
RESULT 12		
UGS2_SOLUTU	STANDARD;	PRT; 641 AA.
AC	P93568;	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Soluble glycogen [starch] synthase, chloroplast precursor	
DE	(EC 2.4.1.11) (SS I).	
OS	Solanum tuberosum (Potato).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.	
OX	NCBI_TaxID=4113;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=cv. Desiree; TISSUE=Leaf;	
RX	MEDLINE=97164391; PubMed=9011082;	
RA	Abel G.J.W., Springer F., Willmitzer L., Kossmann J.;	
RT	"Cloning and functional analysis of a cDNA encoding a novel 139 kDa	
RT	starch synthase from potato (Solanum tuberosum L.)."	
RL	Plant J. 10:981-991(1996).	
CC	-!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =	
CC	UDP + {(1,4)-alpha-D-glucosyl}(N+1).	
CC	-!- PATHWAY: Starch biosynthesis.	
CC	-!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY	
CC	SIMILARITY).	
CC	-!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE	
CC	FAMILY.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; Y10416; CAA71442.1; -	
DR	InterPro; IPR001296; Glycos.transf.1.	
DR	Pfam; PF00534; Glycos.transf.1.	
KW	Glycogen biosynthesis; Transferase; Glycosyltransferase;	
KW	Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.	
FT	TRANSIT 1 ? CHLOROPLAST (POTENTIAL).	
FT	CHAIN ? 641 SOLUBLE GLYCOGEN [STARCH] SYNTHASE.	
FT	BINDING 145 145 UDP-GLUCOSE (BY SIMILARITY).	
SQ	SEQUENCE 641 AA; 70608 MW; 30F8B0546CEFB74C CRC64;	
Query Match 26.8%; Score 902.5; DB 1; Length 641;		
Best Local Similarity 39.8%; Pred. No. 9.9e-47;		

This SWISS-PROT entry is copyright. It is produced through a collaboration


```
QY 503 LLEEVVY 509
Db 744 VLVAARY 750

RESULT 15
UGS2_WHEAT STANDARD; PRT; 610 AA.
AC Q43654;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. T.A. Florida; TISSUE=Endosperm;
RA Block M., Loez H., Lueticke S.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + [(1,4)-alpha-D-glucosyl](N) =
CC UDP + [(1,4)-alpha-D-glucosyl](N+1).
CC -1- PATHWAY: Starch biosynthesis.
CC -1- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; U48227; AAB02197.1;
DR InterPro: IPR001296; Glycos_transf_1.
DR Pfam: PF00534; Glycos_transf_1;
DR Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
FT NON_TER 1 1
FT TRANSIT <1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 610 SOLUBLE GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 7 7 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 610 AA; 67143 MW; 45080A3B7FB87193 CRC64;
```

```
Query Match 25.8%; Score 869; DB 1; Length 610;
Best Local Similarity 35.08; Pred. No. 9.3e-45;
Matches 234; Conservative 94; Mismatches 222; Indels 118; Gaps 22;

QY 10 EVAPWSKTGGIGDYTGGLPIELVKRGHVMYIAPRY-----DOYADAWDTSVVVDIM-- 61
Db 1 EAAPYAKSGGLGDCGSLPIALAAARHVRVMVMPRYLNGSSDKNYAKHYAKHIKIPCF 60

QY 62 --GEKRYFHSIKGVHVRWIDHPWFLAKVWGKTCGLYGRSGADYLDNHRKRALFCKA 119
Db 61 GGSHEVTFFHRYRNDVWVFVDHP-----SYHRFGS-LYGNDFGA-FGDNQFRYTLACYA 113

QY 120 AIEARVLPFGP---GEDCVFVANDHSALVPLLKDEYQPKGQFTKAKSVLAIHNIAPQ 176
Db 114 ACEAPLLELGGYIYGQCMFVNDWHDASLVFLLAAKRYPGYVRDSRSTLVIHNLAHQ 173

QY 177 GRMWEAFKDKLQFAFDKLFASDGYAKVYEAATPMEDEKPLTGKTYKINWLKGGI 236
Db 174 GVPEASTYDGLGLPEWGALEW-----VPEWARRHALDKG-----EAVNELKGA 220

QY 237 IAADKLVTVSPNATEIAADRAAGGVELDTVI--RAKGTGIVNGMDIEWNPKTDKFLSA 294
```

Search completed: June 4, 2003, 14:53:12
Job time : 13.7412 secs

This Page Blank (uspro)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:35:26 ; Search time 32.3424 Seconds
(without alignments)
4147.394 Million cell updates/sec

Title: US-09-980-771a-3_COPY_58_708
Perfect score: 3370
Sequence: 1 ALDIYVAAEAVAPWSKTGGL.....SASKTSAAPLVSAATRKSA 651

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3366	99.9	708	10	O64925 chlamydomon
2	1463.5	43.4	613	10	Q93YB1 pisum sativ
3	1450.5	43.0	604	10	Q9FR03 perilla fru
4	1424.5	42.3	608	10	Q93VD9 ipomoea bat
5	1423.5	42.2	606	10	Q9XIS6 phaseolus v
6	1423.5	42.2	607	10	Q92S05 astragalus
7	1404	41.7	608	10	Q8VYU1 oryza sativ
8	1397.5	41.5	609	10	Q94LY7 oryza sativ
9	1395.5	41.4	603	10	Q8SA49 hordeum vul
10	1390	41.2	610	10	Q9MAQ0 arabidopsis
11	1389.5	41.2	609	10	Q8S9C4 oryza sativ
12	1381	41.0	605	10	Q9SXX3 triticum ae
13	1380	40.9	605	10	Q9FUD6 triticum ae
14	1379	40.9	599	10	Q9SQ58 triticum ae
15	1376	40.8	606	10	Q43012 oryza sativ
16	1375	40.8	604	10	Q9S7N5 triticum ae

17	1371	40.7	534	10	Q9W2G8 triticum ae
18	1369	40.6	604	10	Q9SLS6 triticum tu
19	1367.5	40.6	604	10	Q9SLS7 triticum tu
20	1367	40.6	605	10	Q9SQ51 aegilops sp
21	1366	40.5	605	10	Q9SLS8 triticum tu
22	1362.5	40.4	604	10	Q9SXX4 triticum ae
23	1360.5	40.4	604	10	Q9SLS9 triticum tu
24	1354.5	40.2	605	10	Q9SQ52 triticum mo
25	1353.5	40.2	574	10	Q9SYU0 triticum ae
26	1263.5	37.5	565	10	Q9XEN9 triticum ae
27	898	26.6	792	10	Q9MAC8 arabidopsis
28	895.5	26.6	313	10	Q9LKD3 vaquelinia
29	893.5	26.5	313	10	Q9LKE0 prunus virg
30	893.5	26.5	313	10	Q9FYU8 aruncus dio
31	891.5	26.5	647	10	Q9LEB9 triticum ae
32	891.5	26.5	647	10	Q9SOH0 aegilops ta
33	891.5	26.5	647	10	Q9SQG9 triticum ae
34	890.5	26.4	647	10	Q9LECO kageneckia
35	886.5	26.3	313	10	Q9LKE8 chlamydomon
36	886	26.3	576	10	O64926 exochorda r
37	885.5	26.3	313	10	Q9LKD1 hordeum vul
38	884.5	26.2	643	10	Q9M5A3 amelanchier
39	879.5	26.1	313	10	Q9LKF5 vaquelinia
40	879.5	26.1	313	10	Q9LKD6 kageneckia
41	878.5	26.1	313	10	Q9LKE7 prinsepia s
42	878.5	26.1	313	10	Q9LKE1 malus sarge
43	877.5	26.0	313	10	Q9LKE6 rosa multif
44	877.5	26.0	313	10	Q9LKD8 oemleria ce
45	876.5	26.0	313	10	Q9LKE5

ALIGNMENTS

RESULT 1
O64925 PRELIMINARY; PRT; 708 AA.
AC O64925; 01-AUG-1998 (TREMBLrel. 07, Created
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DI 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Granule-bound starch synthase I precursor (EC 2.4.1.21).
GN STA2
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137C;
RA D'Huist C.; Wattedled F., Ral J.-P., Abel G.J., Kossmann J.,
RA Ball S.G.;
RT "Cloning of a cDNA encoding for the GBSSI in the green alga
RT Chlamydomonas reinhardtii.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wattedled F., Ball S.G., D'Huist C.;
RT "Granule-bound starch synthase I: A major enzyme involved in the
RT biogenesis of B-crystallites in starch granules.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF026420; AAC17969.3;
DR EMBL; AF433156; AAL28128.1;
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR002114; HPR_Serp.site.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
KW Glycosyltransferase; Transferrase; Transit peptide.
FT TRANSIT 1 57 POTENTIAL.
FT CHAIN 58 708 GRANULE-BOUND STARCH SYNTHASE I.
SQ SEQUENCE 708 AA; 74623 MW; 7D2A5A07D8606469 CRC64;

Query Match 99.9%; Score 3366; DB 10; Length 708;

Best local Similarity 99.8%; Pred. No. 4.5e-190;
Matches 650; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALDIWVAEAVAPWSKTGGLGDTGGLPIELVKRGRVMTIAPRYDQYADADMTSVVVDI 60
DB 58 ALDIWVAEAVAPWSKTGGLGDTGGLPIELVKRGRVMTIAPRYDQYADADMTSVVVDI 117

QY 61 MGEKVRYPHSIKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKFAFCRAA 120
DB 118 MGEKVRYPHSIKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKFAFCRAA 177

QY 121 IEAARVLPFGEGDCVFAVDWHSALVPVLKDEYQPKGQSTKAKSVLAIHNIAPQGRMW 180
DB 178 IEAARVLPFGEGDCVFAVDWHSALVPVLKDEYQPKGQSTKAKSVLAIHNIAPQGRMW 237

QY 181 EEAFKDNLKPOAEFKLAFSDGYAKVYTEATPMEDEKPLTGTGTYKKNLKGGLIAAD 240
DB 238 EEAFKDNLKPOAEFKLAFSDGYAKVYTEATPMEDEKPLTGTGTYKKNLKGGLIAAD 297

QY 241 KLVTSPNYATEIAADAAGGVELDTVIRAKIEGIVNGMDIEENPKTDKFLSAPYDONS 300
DB 298 KLVTSPNYATEIAADAAGGVELDTVIRAKIEGIVNGMDIEENPKTDKFLSAPYDONS 357

QY 301 VYAGKAAKALQALGELGDPVDTAPLFAFGRLEEGKGVDTIILALPKILATPKVQTAIL 360
DB 358 VYAGKAAKALQALGELGDPVDTAPLFAFGRLEEGKGVDTIILALPKILATPKVQTAIL 417

QY 361 GTGKAAEYKLVNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVPSRFPCCGLIQLHAM 420
DB 418 GTGKAAEYKLVNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVPSRFPCCGLIQLHAM 477

QY 421 HYGTVPVVASTGGVLDVTKGCVTFHMGALNPDKLDEADADALAAATVRRASEVPAGGRYP 480
DB 478 HYGTVPVVASTGGVLDVTKGCVTFHMGALNPDKLDEADADALAAATVRRASEVPAGGRYP 537

QY 481 EMVANCISQDLSWSKPAQKWEGLLEEVYKGGVATAKKEIKVPVAKETPGDLPVASYA 540
DB 538 EMVANCISQDLSWSKPAQKWEGLLEEVYKGGVATAKKEIKVPVAKETPGDLPVASYA 597

QY 541 PNTLKPVASVEGNGAAAPKVGTTAPAMGAWRATTSGSPSAAATPKVTTYKPALPATAK 600
DB 598 PNTLKPVASVEGNGAAAPKVGTTAPAMGAWRATTSGSPSAAATPKVTTYKPALPATAK 657

QY 601 PRTAGLKLAGEASTTSTSENGASNGNGCASASKTSAKPLVSAATRKA 651
DB 658 PRTAGLKLAGEASTTSTSENGASNGNGCASASKTSAKPLVSAATRKA 708

RESULT 2

Q93YB1 PRELIMINARY; PRT; 613 AA.

AC Q93YB1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Granule-bound starch synthase (EC 2.4.1.11).
GN GBSSI.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. OKDONG; TISSUE=DEVELOPING SEEDS;
RA Edwards A., Vincken J.P., Visser R., Zeeman S., Smith A.M., Martin C.;
RT "Discrete forms of amylose are synthesised by isoforms of GBSSI in pea".
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ345045; CAC69955.1;
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR001917; NHtransf_2.
DR Pfam; PF00534; Glycos_transf_1; 1.

DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
KW Glycosyltransferase; Transferase; Transit peptide.
FT TRANSIT 1 85
FT CHAIN 86 613 GRANULE BOUND STARCH SYNTHASE.
SQ SEQUENCE 613 AA; 67626 MW; 5A653461128F97EB CRC64;

Query Match 43.4%; Score 1463.5; DB 10; Length 613;
Best Local Similarity 53.0%; Pred. No. 4.1e-78;
Matches 291; Conservative 74; Mismatches 137; Indels 47; Gaps 11;

QY 2 LDIVMVAEAVAPWSKTGGLGDTGGLPIELVKRGRVMTIAPRYDQYADADMTSVVVDI- 60
DB 87 MNLIEVGTAVAPWSKTGGLGDTGGLPALSANGHRVMTIAPRYDQYADADMTNTIEVK 146

QY 61 ---MGEKVRYPHSIKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKFAFC 117
DB 147 VGDRTKVRFFCHFCRGVDFVDFHPIFLKRVGKTGTLKYGPAAGDDYQDNOLRFSIFC 206

QY 118 KAAIEAARVLPF-----GP-GEDEVFANDWHSALVPVLKDEYQPKGQSTKAKSVLA 169
DB 207 QAAIEAARVNLKSNKYFSGPYGDEVFVANDWHSALVSCYKMSYQSIGIFRNKVVFC 266

QY 170 IHNIAFOGRMWEAFKD---TKLPQAAFDKLFSDGYAKVYTEATPMEDEKPLTGTGTY 226
DB 267 IHNIAFOGRF---AFTDYSILNLPDQPKSFDGLDGHVK-----PIVG--- 306

QY 227 KKNLWKGGLIAADKLVTSPNYATEIAADAAGGVELDTVIRAKIEGIVNGMDIEENPK 286
DB 307 KKNLWKGGLIAADKLVTSPNYATEIAADAAGGVELDTVIRAKIEGIVNGMDIEENPK 366

QY 287 KTDKFLSAPYDONSQVYAGKAAKALQALGELGDPVDTAPLFAFGRLEEGKGVDTIILAL 346
DB 367 STDKYISIKYDASTVLEGKALLKEELQAEVCLPDKVNPVLIAPLGRLEEGKGSLLVFAI 426

QY 347 PKILATPKVQTAILGTCGAAYEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADFMVLP 406
DB 427 PQFI-KENVQIVALTGKTKEMEKQLOQLLEISYDPKARGVAKFNVPVLAHMTAGADFIILP 485

QY 407 SRPEPCGLIOLHAMHYGTVPVWASTGGVLDVTKGCVTFHMGALNP--DKLDEADADALA 464
DB 486 SRPEPCGLIOLHAMHYGTVPVWASTGGVLDVTKGCVTFHMGALNP--DKLDEADADALA 545

QY 465 ATVRRASEVPAGGRYPVEMVANCISQDLSWSKPAQKWEGLL-----EEVYKGGVAT 516
DB 546 KTVTKALGVYGTSAFAEDMIKNCMAQELSWKPAKKEEVLNLCVDPSEPDGQ-BIAP 604

QY 517 AKKEIKVP 525
DB 605 QAKENVATP 613

RESULT 3

Q9FR03 PRELIMINARY; PRT; 604 AA.

AC Q9FR03;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Granule-bound starch synthase.
GN GBSSI.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. OKDONG; TISSUE=DEVELOPING SEEDS;
RA Hwang S.-K., Hwang Y.-S.;
RT "Isolation and characterization of a cDNA encoding granule-bound starch synthase from perilla frutescens".
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210699; AAG43519.1; -.

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB029546; BAA82346.; -
 DR InterPro; IPR001296; Glycos_transf.1.
 DR Pfam; PF00534; Glycos_transf.1; 1.
 KW Glycosyltransferase; Transferase; Transit peptide.
 FT TRANSIT 1 78 POTENTIAL
 SQ SEQUENCE 606 AA: 67080 MW: 246943.30
 ...

[illegible]

RESULT 6	Q9ZSQ5	PRELIMINARY;	PRT;	607 AA.
ID	Q9ZSQ5			
AC	Q9ZSQ5;			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	Granule-bound glycogen (starch) synthase (EC 2.4.1.11).			
OS	Astragalus membranaceus (Milk vetch) (Huang qi).			
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosids I; Fabales; Fabaceae; Papilionoideae; Galegeae; Astragalus.			
OX	NCBI_TaxID=83837;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE-HAIRY ROOTS INDUCED BY RHIZOGENESIS AGROBACTERIUM LB49402;			
RA	Peng J.S., Liu D., Hu Z.B.;			
RT	"CDNA cloning and structural analysis of granule-bound starch synthase			
RT	gene of Astragalus membranaceus.";			
RL	Submitted (06-1998) to the EMBL/GenBank/DBJ databases.			

```
DR EMBL; AF097922; AAC70779.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR PFam; PF00534; Glycos_transf_1; 1.
DR KW Glycosyltransferase; Transferase.
DR SQ SEQUENCE 607 AA; 66560 MW; 61EB0CAC94D387C CRC64;
```

Query Match	42.2%	Score 1423.5	DB 10	Length 607
Best Local Similarity	52.7%	Pred. No. 9.1e-76		
Matches 289	Conservative 74	Mismatches 140	Indels 45	Gaps 12
QY	2	LDIVMAAEAPAPSKTGGGLGVTGGPLFELVKGHRVMTIAPRYDQADAWDTSVVVDI- 60		
Db	81	MNLVFCVGAEGPWSKTGGGLGDLVGLPPALAGNGHRVMTSPRYDQYKDAWDIGVSVEIK 140		
QY	61	MG---EKVRFHSIKKGVRHWIDHFWFLAKVNGKGTGSKLYGPRSGADYLDNHNKRFALFC 117		
Db	141	VGRDFEVRFFHCYKRGVDVRFVDHPLFLSEKVMGTESKLYGPKTYGVDYKDNQLRFSLLC 200		
QY	118	KAATEARVLFF-----GP-GEDECVFVANDMHSALVPVLLKDEYQPKQGFQTKASVLA 169		
Db	201	QAALAPRVNLNLSNKHFSGPYGEDVVFVANDMHTALLPCYLSKSLYKSGIYKSAAVFC 260		
QY	170	IHNIAFGRMWEZAFKD---TKLPOAADFKLAFSDGKAVKYTTEATPMEDEKEPPLTKYI 226		
Db	261	IHNIAVQGR---HAFSDLILLNLPNFRSDFDIDGTDK-----PVGK--- 300		
QY	227	KKINWIKGGIIAADKLVTSNPYATEIAADPAGGVBLDTVIRAKGTIEGVNGMDIEWNP 286		
Db	301	RKINMKAGVLESDFRYTSPYAKELVSGEDRGVELDNIIRSIGTIGVNGMDNREWSF 360		
QY	287	KTDKFLSAPYDQNSVYAGKAAKEALQAEGLGVPDPTAPLFAFIFGLEQKGVDIILAAL 346		
Db	361	QTDRYIDVHDASTVTTEAKALKEALQAEVGLPVDNRNIPVIGFIRGLEQKGSIIIVESI 420		
QY	347	PKLIATPKVQIAILGTGKAAAYEKLVNAIGTKYKGRAGKVVYKSPASLAHMLTLAGDFMLVP 406		
Db	421	PKFI-DQNYOIIVLGTGKKIMKQIQLEWTEVTPGKAIGVAKFNPSPLAHLKIAGADPIVP 479		
QY	407	SFPECGLLIQLHAMHYGTVPVYVASTGGLVDYTKEGVTGFHMGALNP--DKLDEADADALA 464		
Db	480	SFPECGLVOLHAMPTGTVPVYSSTGGLVDYTKEGYTGPHVGAFSVECEAVDPADVEKLA 539		
QY	465	ATVIRASEVTFAGRPPEMVANICISQDLSKSPAQKWEGLL--EEVYVYGGK-----VATA 517		
Db	540	TTVNALKTYGTQALKMILNCMAQDFSWKGPAKOWEQALLSLEVAGSEPPGIDGEEVAPL 599		
QY	518	KKEEIKVP 525		
Db	600	AKENVATP 607		

```

RESULT 7
Q8VYU1
ID Q8VYU1 PRELIMINARY; PRT; 608 AA.
AC Q8VYU1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Granule binding starch synthase II.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RA Wu P., Dian W.M., Jiang H.W.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AY069940; AAL38572.1; -.
DR Interpro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1.
SQ SEQUENCE 608 AA; 67327 MW; D96066254E9400E CRC64.

```


Matches 277; Conservative 71; Mismatches 141; Indels 31; Gaps 7;	
QY	2 LDIYVAAEAVAPWSKTGGLGVDVTGGLPIELVKRGHRVMTIAPRYDOYADAMDTSVVVDIM 61
DB	76 MNLVFGAEMAPWSKTGGLGVDVGLGGLPAMAANGHRVNVSPRIDQYKADAMDTSVISIK 135
QY	62 ---GEKRYFHSIKKGVHRVWIDHPFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
DB	136 VADEYERYFFHCYKRGVDVFDHPWLEKVRCKTEKIYGPDAITDYEDNQRFSLIC 195
QY	118 KAAIEAAKVL-----PF--GP-GECDVFNWDSHSAIPLVLLKDIYQKQGTAKSVLA 169
DB	196 QAAIEAPRILNINNPFESGYPGEDVDFVFNWDSHSAIPLVLLKDIYQKQGTAKSVLA 255
QY	170 IHNIAFOGMEWEEAFKDKLP--QAADFCLAFSDGYAKVYTEATPMEDEKPPLTGKTY 229
DB	256 IHNISYQGRSFDDFAQLNLPDRFKSSFDIDYDK-----PVEG---RKI 298
QY	230 NMLKGGIIAADKLVTVPSPNYATEIAADAAGGVVELDTVIRAKGIEGIVNGMDIEEWNPKTD 289
DB	299 NNMKAGILQADKVLTVSPYAEELISGEARGCELDNIMRLTGITGIVNGMDVSEWDPTKD 358
QY	290 KFLSAPYDONSIVAGKAAKAEALQAEGLPVDPTAPLFAFISGLEEQKGVDDIILAALPKI 349
DB	359 KFLAVNYDITTALEAKALNKEALQAEVGLPVDKVPVAFISGLEEQKGVDDIILAALPKI 418
QY	350 LATPKVQIATLGTGKAAYEKLNAIGTKYKGRAGKGVKFSAPLAHMLTAGADFMVPSRF 409
DB	419 LKEEDVQIILLGTGKKEFKLKSMEEFPGKRVAVRVPNAPLAHMLTAGADFMVPSRF 478
QY	410 EPCGLIQLHAMHYGTPVVPVASTGGLVDTYKGVTFGFMGALNPD--KLDEADADALAATV 467
DB	479 EPCGLIQLHAMHYGTPVVPVASTGGLVDTYKGVTFGFMGALNPD--KLDEADADALAATV 538
QY	468 RRASEVFAGGRYPPEMVANCISQDLSWSKPAQKWEGLLEEV 507
DB	539 KRAVKYVGTGTPAYQEMVKNCMIQDLSWKGPKNWEDVLEL 578
RESULT 10	
Q9MAQ0	PRELIMINARY; PRT; 610 AA.
ID	Q9MAQ0
AC	Q9MAQ0
DT	01-OCT-2000 (TREMBlrel. 15, Created)
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE	Granule-bound starch synthase.
FN	F9L11.8.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. COLOMBIA;
RA	Pederspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA	Altati H., Nguyen M., Lam B., Southwick A., Bei, Buehler E., Chin C.,
RA	Chiou J., Choi E., Dunn P., Gonzalez A., Howing B., Kim C., Koo T.,
RA	Lee J.M., Ienz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
RA	Pham P., Sakano H., Schwartz J., Shinn P., Thaveri A., Toriumi M.,
RA	Vaysberg M., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AC006424; AAF31273.1;
DR	InterPro: IPR001296; Glycos.transf_1.
DR	Pham; PF00534; Glycos.transf_1; 1.
SQ	SEQUENCE 610 AA; 66879 MW; CF17F25BE12220DF CRC64;
Query Match 41.2%; Score 1390; DB 10; Length 610;	
Best Local Similarity 52.7%; Pred. No. 8.6e-74;	
Matches 287; Conservative 72; Mismatches 146; Indels 40; Gaps 12;	
QY	2 LDIYVAAEAVAPWSKTGGLGVDVTGGLPIELVKRGHRVMTIAPRYDOYADAMDTSVVVDI- 60

Matches 277; Conservative 71; Mismatches 141; Indels 31; Gaps 7;	
DB	84 MSVFIGAEVGSWSTGGLGVDVGLGGLPALAARGHRVMTICPRIDQYKADAMDTSVVQIK 143
QY	61 MGEK---VRYFHSIKKGVHRVWIDHPFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
DB	144 VGDKYENVRFFHCYKRGVDVFDHPFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 203
QY	118 KAAIEAAKVL-----GP-GECDVFNWDSHSAIPLVLLKDIYQKQGTAKSVLA 169
DB	204 QAAIEAPQVNLNNSKYSFGYPGEDVDFVFNWDSHSAIPLVLLKDIYQKQGTAKSVLA 263
QY	170 IHNIAFOGMEWEEAFKDKLP--QAADFCLAFSDGYAKVYTEATPMEDEKPPLTGKTY 226
DB	264 IHNIAFOGMEWEEAFKDKLP--QAADFCLAFSDGYAKVYTEATPMEDEKPPLTGKTY 303
QY	227 KKNLWKGIIAADKLVTVPSPNYATEIAADAAGGVVELDTVIRAKGIEGIVNGMDIEEWNPKTD 286
DB	304 RKNWKAALAEHVRVTVSPYAEELISGEARGVHELKYLKMTVSGIINGMDVQEWNP 363
QY	287 KTDKFLSAPYDONSIVAGKAAKAEALQAEGLPVDPTAPLFAFISGLEEQKGVDDIILAAL 346
DB	364 STDKYIDIKYDITTTVDKAPLKEALQAAVGLPVDKVPVAFISGLEEQKGVDDIILAAL 423
QY	347 PKILATPKVQIATLGTGKAAYEKLNAIGTKYKGRAGKGVKFSAPLAHMLTAGADFMVPSRF 406
DB	424 SFPMGL-NYOMVILGTGKKEFKLKSMEEFPGKRVAVRVPNAPLAHMLTAGADFMVPSRF 482
QY	407 SRFPCGLIQLHAMHYGTPVVPVASTGGLVDTYKGVTFGFMGALNPD--KLDEADADALA 464
DB	483 SRFPCGLIQLHAMHYGTPVVPVASTGGLVDTYKGVTFGFMGALNPD--KLDEADADALA 542
QY	465 AIVRRASEVFAGGRYPPEMVANCISQDLSWSKPAQKWEGLLEEVYVYGGVATAKKEIKV 524
DB	543 KAVTRAVAVGTSGAMQEMVKNCMQDQFSWKGPARLWKEVLLSLNVA-GSEAGTEGBEI-A 600
QY	525 PVAEK 529
DB	601 PLAKE 605
RESULT 11	
Q8S9C4	PRELIMINARY; PRT; 609 AA.
ID	Q8S9C4
AC	Q8S9C4
DT	01-JUN-2002 (TREMBlrel. 21, Created)
DT	01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE	Starch granule-bound starch synthase.
FN	WX-1.
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Ehrhartideae; Oryzeae; Oryza.
OX	NCBI_TaxID=4530;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. MILKY QUEEN;
RA	Sato H., Suzuki Y., Sakai M., Imbe T.;
RT	"Molecular Characterization of wx-1, a Novel Mutant Gene for Low-
RT	amylose Content in Endosperm of Rice (Oryza sativa L.).";
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AB066093; BAB88209.1;
SQ	SEQUENCE 609 AA; 66431 MW; B57CC13E0440D227 CRC64;
Query Match 41.2%; Score 1389.5; DB 10; Length 609;	
Best Local Similarity 51.2%; Pred. No. 9.2e-74;	
Matches 280; Conservative 76; Mismatches 148; Indels 43; Gaps 9;	
QY	2 LDIYVAAEAVAPWSKTGGLGVDVTGGLPIELVKRGHRVMTIAPRYDOYADAMDTSVVVDI- 60
DB	83 MNVYVGAEMAPWSKTGGLGVDVGLGGLPAMAANGHRVNVISPRYDQTKDAMDTSVVAEIK 142
QY	61 ---MGEKRYFHSIKKGVHRVWIDHPFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117

Db 143 VADRYVERFEHCYKHGVDVDFIDHPSELEKVGKGTGKIYGDPTGVHDKDMQMFSLC 202
 QY 118 KAAIDAAVUL-----PFGP-----GDCVFNVDHWSALVPVLKDEYQPKQFTAKSVLA 169
 Db 203 QAALEAPRILNINNPNYFKGTGDEWVFCNDWHGTPLASYLKNNYQNGIYRNAKVAFC 262
 QY 170 IHNIAFOGRMEEAFKDTKLQAAFDKLAFSQYAKVYTEATPMEDEKPPLTGTYKKI 229
 Db 263 IHNISYQGRFAFEDYPELNLSERFRSPDFIDGY-----DTPVEG-----RKT 305
 QY 230 NMLKGGIITADKLVTVSPNYATEIAADAAGGVLDVIRAKGIEGIVNGMDIEENPKTD 289
 Db 306 NNMKAGILEADRLTVSPVYAEELISGTARGCELDINMLTGITGIVNGMDVSEWDPK 365
 QY 290 KFLSAPYDONSYYAGKAAKAEALQAEGLPVDPTAPLFAFTGRLEEQKGVDIILAAALPKI 349
 Db 366 KIITAKYDATTAEAKALNKEALQAEAGLPVDRKIPILTAFTGRLEEQKGVDPVMAAIPEL 425
 QY 350 LATPKVQITAILGTGKAAVEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMLVPSRF 409
 Db 426 M-QEDVQIVLLGTGKKFEKLLKSWEEKYPKVRVVFKNAPLAHMLTAGADFMLVPSRF 484
 QY 410 EPCGLIQLHAMHYGTPVPVASTGGLVDTVKEGVTGFHMGALNPD--KLDEADADALAATV 467
 Db 485 EPCGLIQLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDCVKVPESDVKVVAATL 544
 QY 468 RRASEVFAAGGRYPPEMVANCISODLSWSKPAQKWEGLLEEVYVYGGK-----VATAK 518
 Db 545 KRAIKVGTPTAYEENVRNMCNODLSWKGPAKNWENVL--LGLGVAGSAPGIEGDEIAPLA 602
 QY 519 KEEKVP 525
 Db 603 KENVAAP 609

RESULT 12

Q9SXK3 ID Q9SXK3 PRELIMINARY; PRT; 605 AA.
 AC Q9SXK3;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Starch synthase (GBSSI) (EC 2.4.1.21).
 GN WAXY.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99321800; PubMed=10393240;
 RA Murai J., Taira T., Ohta D.;
 RT "Isolation and characterization of the three waxy genes encoding the
 granule-bound starch synthase in hexaploid wheat."
 RL Gene 234:71-79(1999).
 DR EMBL; AB019623; BAA77351.1; .
 DR InterPro; IPR001296; Glycos_transf_1.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 605 AA; 66345 MW; 60A816276F78722B CRC64;

Query Match 41.0%; Score 1381; DB 10; Length 605;
 Best Local Similarity 51.5%; Pred. No. 2.9e-73;
 Matches 281; Conservative 72; Mismatches 153; Indels 40; Gaps 9;
 QY 2 LDIWVAAEAVAPSKTGGGLGDTVGGPLPIELVKRGHVMYTIAPRYDQYADAWDTSVVVDIM 61
 Db 78 MNLVFGAEMAPWSKTGGGLGDLGLGPPAMAANGHRVMYISPRYDQYKDAWDTSVYSEIK 137

QY 62 ----GEKVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
 Db 138 VADRYVERFEHCYKHGVDVDFIDHPSELEKVGKGTGKIYGDPTGVHDKDMQMFSLC 197
 QY 118 KAAIDAAVUL-----PFGP-----GDCVFNVDHWSALVPVLKDEYQPKQFTAKSVLA 169
 Db 203 QAALEAPRILNINNPNYFKGTGDEWVFCNDWHGTPLASYLKNNYQNGIYRNAKVAFC 262
 QY 170 IHNIAFOGRMEEAFKDTKLQAAFDKLAFSQYAKVYTEATPMEDEKPPLTGTYKKI 229
 Db 263 IHNISYQGRFAFEDYPELNLSERFRSPDFIDGY-----DTPVEG-----RKT 305
 QY 230 NMLKGGIITADKLVTVSPNYATEIAADAAGGVLDVIRAKGIEGIVNGMDIEENPKTD 289
 Db 306 NNMKAGILEADRLTVSPVYAEELISGTARGCELDINMLTGITGIVNGMDVSEWDPK 365
 QY 290 KFLSAPYDONSYYAGKAAKAEALQAEGLPVDPTAPLFAFTGRLEEQKGVDIILAAALPKI 349
 Db 366 KIITAKYDATTAEAKALNKEALQAEAGLPVDRKIPILTAFTGRLEEQKGVDPVMAAIPEL 425
 QY 350 LATPKVQITAILGTGKAAVEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMLVPSRF 409
 Db 426 M-QEDVQIVLLGTGKKFEKLLKSWEEKYPKVRVVFKNAPLAHMLTAGADFMLVPSRF 484
 QY 410 EPCGLIQLHAMHYGTPVPVASTGGLVDTVKEGVTGFHMGALNPD--KLDEADADALAATV 467
 Db 485 EPCGLIQLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDCVKVPESDVKVVAATL 544
 QY 468 RRASEVFAAGGRYPPEMVANCISODLSWSKPAQKWEGLLEEVYVYGGK-----VYKGGVATAKK 519
 Db 545 KRAIKVGTPTAYEENVRNMCNODLSWKGPAKNWENVL--LGLGVAGSAPGIEGDEIAPLA 599
 QY 520 KEEKVP 525
 Db 600 ENVAAP 605

RESULT 13

Q9FUU6 ID Q9FUU6 PRELIMINARY; PRT; 605 AA.
 AC Q9FUU6;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Granule bound starch synthase I (EC 2.4.1.21).
 GN GBSSI.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. CHEYENNE; TISSUE=ENDOSPERM;
 RA McCue K.F., Hurkman W.J., Tanaka C.K., Anderson O.D.;
 RT "Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum
 cv. Cheyenne): Molecular Characterization, Developmental Expression,
 and Homolog Assignment by Differential PCR."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF286320; AAG27624.1; .
 DR InterPro; IPR001296; Glycos_transf_1.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 605 AA; 66326 MW; 21120D9D6F68B891 CRC64;

Query Match 40.9%; Score 1380; DB 10; Length 605;
 Best Local Similarity 51.5%; Pred. No. 3.3e-73;
 Matches 281; Conservative 72; Mismatches 153; Indels 40; Gaps 9;
 QY 2 LDIWVAAEAVAPSKTGGGLGDTVGGPLPIELVKRGHVMYTIAPRYDQYADAWDTSVVVDIM 61
 Db 78 MNLVFGAEMAPWSKTGGGLGDLGLGPPAMAANGHRVMYISPRYDQYKDAWDTSVYSEIK 137

Db 78 MNLVFGAEMAPWSKTGGGLDVLGGLPPAMAANGHRVMVISPRYDQYKDAWDTSVVSEIK 137
 QY 62 ---GEKVYFHSIKGVHVRWIDHPWFLAKYWGKTSKLYGPRSCADYLDNHRKFAFC 117
 Db 138 VADEYERVFYHCYKRGVDRVFDHPFCFELEKRGKTKYKIYGPDAQDYEDNQLRSLC 197
 QY 118 KAAIEAARVL-----PF--GP--GEDCVFVANDHWSALVPLVLLKDEYQPKQGTAKASVLA 169
 Db 198 QAALAPRILDLNNPYSFGPYGVEDVFCNDHHTGLLACYLKSNSQSSGIYRTAKVAEC 257
 QY 170 IHNIAPQGRMWEAEAFKDTKLPOAAFDKLAFLSDGYAKVYITEATPMEDEKPLTGKTKYKI 229
 Db 258 IHNISYQGRFSFDDFAQLNLPDRFKSSFDIDGYDK-----PVEG---RKI 300
 QY 230 NMLKGGIIAADKLVTVPSPNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEEWNPKTD 289
 Db 301 NNMKAGILOADKLVTVSPYAEELISGEARGCELDNIMRLTGITGIVNGMDVSEWDPADK 360
 QY 290 KFLSAPYDONSIVYAGKAAAEALQAEGLPLVDPTAPLFAFIFGRLEBKQGYDITLAALPKI 349
 Db 361 KFLAANYDYTTALEGKALNKEALQAEVGLPVDKVPFLVAFIGRLEBKQGYDVMIAAPEI 420
 QY 350 LATPKVOIALGTGKAAAEKLVNAIGTKYKGRAGKGVVKSAPLAHMLTAGADFMVPSRF 409
 Db 421 LKEEDVQIVLLGTGKKKKFERLLKSVEEKFPSKRVAVVRFNAPLAHOMAGADVAVTSRF 480
 QY 410 EPCGLIQLHAMHYGTVPVVASTGGLVDTYKGVTFGFMGALNPD--KLDEADADALAATV 467
 Db 481 EPCGLIQLGOMRYGTPCACASTGGLVDTIMEGKTGFHMGHLSVDCNVVEPADVKVVTIL 540
 QY 468 RRASEVFAAGRYPEMVCANSODLSWSKPAQKWEGLLEEV-----YVGKGVGATAKK 519
 Db 541 KRAVKVGTGPAYHEMVKMNCMIODLSWKGPAKNEDVILELGVGESEPGVIGE-EIAPLAM 599
 QY 520 EETKVP 525
 Db 600 ENVAAP 605

RESULT 14
 Q9SQ58 PRELIMINARY; PRT; 599 AA.
 ID Q9SQ58
 AC Q9SQ58;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Granule-bound starch synthase GBSSII.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakamura T., Vrinten P.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF109395; AAF14233.1;
 DR InterPro; IPR001296; Glycos_transf_1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 599 AA; 66045 MW; D486EFC90557F131 CRC64;

Query Match 40.9%; Score 1379; DB 10; Length 599;
 Best Local Similarity 50.4%; Pred. No. 3.7e-73;
 Matches 277; Conservative 78; Mismatches 147; Indels 48; Gaps 10;

QY 2 LDIVWAAEAPWSKTGGGLDVLGGLPPAMAANGHRVMVISPRYDQYKDAWDTSVVVDIM 61
 Db 72 MPILFVTEVHPWCKTGGLGVGGLPPALAAAMGHRVMTAPRYDQYKDAWDTNVLVEVI 131
 QY 62 ---GEKVYFHSIKGVHVRWIDHPWFLAKYWGKTSKLYGPRSCADYLDNHRKFAFC 117
 Db 132 VGDRTVRFPHCYKRGVDRVFDHPFCFELEKRGKTKYKIYGPDTGDFRDNQLRSLC 191

QY 118 KAAIEAARVLPF-----GP--GEDCVFVANDHWSALVPLVLLKDEYQPKQGTAKASVLA 169
 Db 192 LAALAPRILDLNNPYSFGPYGVEDVFCNDHHTGLLACYLKSNSQSSGIYRTAKVAEC 251
 QY 170 IHNIAPQGRMWEAEAFKDTKLPOAAFDKLAFLSDGYAKVYITEATPMEDEKPLTGKTKYKI 229
 Db 252 IHNIAYQGRFPRVDFELLNLPESFMPFSDFVCGHVK-----PVG---RKI 294
 QY 230 NMLKGGIIAADKLVTVPSPNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEEWNPKT 288
 Db 295 NNMKAGITCEDVVLTVSPHYVKELTSPEKGVGLDGLVLRKPLETGIVNGMDVVDWNPAT 354
 QY 289 DKFLSAPYDONSIVYAGKAAAEALQAEGLPLVDPTAPLFAFIFGRLEBKQGYDITLAALPK 348
 Db 355 DKYISYKYNATTVAERALKNEILQAEVGLPVDSSIPVIVFIFGRLEBKQGYDITLAALPK 414
 QY 349 ILATPKVOIALGTGKAAAEKLVNAIGTKYKGRAGKGVVKSAPLAHMLTAGADFMVPSR 408
 Db 415 FL-EENVQIIIVLGTGKKKKEEELMLFAKYPQARGIAKFNVLAHMMFAGANFIIVPSR 473
 QY 409 FEPGGLIQLHAMHYGTVPVVASTGGLVDTYKGVTFGFMGALNP--DKLDEADADALAAT 466
 Db 474 FEPGGLIQLGOMRYGTPICSTGGLVDTYSEGVTFGFMGSFNVFETVDPADVAASVN 533
 QY 467 RRASEVFAAGRYPEMVCANSODLSWSKPAQKWEGLLEEVYKCG-----GVA 515
 Db 534 VTRALKQYKTPSFHAMVQNCMAQDLSWKGPAKKW---EALLGLGVGEQSGLEGGEIA 589
 QY 516 TAKKEIKVP 525
 Db 590 PLAKQNVATP 599

RESULT 15
 Q43012 PRELIMINARY; PRT; 606 AA.
 ID Q43012
 AC Q43012;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Starch granule-bound starch synthase (EC 2.4.1.11).
 GN WAXY.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SSP. L.F. SPONTANEA;
 RA Wang Z.Y., Zheng F.Q., Gao J.P., Wang X.Q., Wu M., Zhang J.L.,
 RA Hong M.M.;
 RT "Identification of two transposon-like elements in rice wx gene."
 RL Sci. China B 37:437-447(1994).
 DR EMBL; X64108; CAA45472.1;
 DR InterPro; IPR001296; Glycos_transf_1.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 606 AA; 66323 MW; E1157468A5553CE CRC64;

Query Match 40.8%; Score 1376; DB 10; Length 606;
 Best Local Similarity 50.7%; Pred. No. 5.7e-73;
 Matches 277; Conservative 77; Mismatches 148; Indels 44; Gaps 10;

QY 2 LDIVWAAEAPWSKTGGGLDVLGGLPPAMAANGHRVMVISPRYDQYKDAWDTSVVVDI- 60
 Db 83 MNVFGAEMAPWSKTGGGLDVLGGLPPAMAANGHRVMVISPRYDQYKDAWDTSVVAEIK 142
 QY 61 ---MGEKVYFHSIKGVHVRWIDHPWFLAKYWGKTSKLYGPRSCADYLDNHRKFAFC 117
 Db 143 VADRYERVRFFHCYKRGVDRVFDHPFCFELEKRGKTKYKIYGPDTGVDYKQNMRFSLC 202

Search completed: June 4, 2003, 14:55:56
Job time : 36.3424 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:49:26 ; Search time 11.5821 Seconds
(without alignments)
1653.790 Million cell updates/sec

Title: US-09-980-771A-3_COPY_58_708

Perfect score: 3370

Sequence: 1 ALDINVVAEFAVPWSKTGGL.....SASKTSAAKPLVSAATRKSA 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/6C.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397.5	41.5	609	3	US-08-941-445A-7
2	1360.5	40.4	600	4	US-09-388-743-22
3	1353.5	40.2	533	3	US-08-941-445A-5
4	1342.5	39.8	616	4	US-09-388-743-14
5	1315	39.0	614	4	US-09-388-743-18
6	1314.5	39.0	615	4	US-09-388-743-2
7	902.5	26.8	641	4	US-08-836-567-10
8	882.5	26.2	649	4	US-09-192-909-2
9	881	26.1	671	4	US-09-196-390-2
10	873	25.9	801	4	US-09-388-743-26
11	871	25.8	767	4	US-08-836-567-8
12	861.5	25.6	539	3	US-08-941-445A-21
13	861.5	25.6	583	3	US-08-941-445A-13
14	858	25.5	690	4	US-09-388-743-6
15	845	25.1	558	4	US-08-836-567-6
16	841	25.0	799	4	US-09-196-390-6
17	837	24.8	698	3	US-08-941-445A-11
18	776	21.5	459	4	US-08-836-567-4
19	701.5	20.8	669	3	US-08-941-445A-9
20	580	17.2	477	1	US-07-735-065-2
21	580	17.2	477	1	US-08-469-202-12
22	580	17.2	477	2	US-08-484-434C-12
23	568.5	16.9	677	4	US-08-836-567-2
24	568.5	16.9	1197	4	US-08-836-567-12
25	568.5	16.9	1230	2	US-08-968-542C-35
26	545	16.2	735	4	US-09-115-704-2
27	530.5	15.7	533	4	US-09-388-743-10

28 504 15.0 1674 2 US-08-968-542C-12
29 240 7.1 64 2 US-08-470-720-15
30 215.5 6.4 79 2 US-08-470-720-13
31 145.5 4.3 2035 1 US-08-046-585-5
32 145.5 4.3 2035 1 US-08-393-703-5
33 145.5 4.3 2035 5 PCT-US93-11721-5
34 143.5 4.3 59 2 US-08-470-720-14
35 134.5 4.0 1222 2 US-08-682-517-15
36 134.5 4.0 1252 2 US-08-682-517-9
37 132 3.9 520 4 US-09-000-016-7
38 132 3.9 520 4 US-09-514-340-7
39 132 3.9 734 4 US-09-000-016-4
40 132 3.9 734 4 US-09-514-340-4
41 132 3.9 823 4 US-09-000-016-2
42 132 3.9 823 4 US-09-514-340-2
43 129 3.8 30 2 US-08-470-720-9
44 129 3.8 1125 4 US-09-513-783A-152
45 129 3.8 1610 4 US-09-513-783A-22

ALIGNMENTS

RESULT 1
US-08-941-445A-7
; Sequence 7, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8089
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-941-445A-7

Query Match 41.5%; Score 1397.5; DB 3; Length 609;
Best Local Similarity 51.4%; Pred. No. 1.4e-113;
Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;
QY 2 LDIVYAAEVAFPWSKTGGLGVDTGGTPIELVKRGRHMTIAPRYDQYADAWDTSVVYDI- 60
Db 83 MNVVFYGAEMAPWSKTGGLGVDTGGTPIELVKRGRHMTIAPRYDQYADAWDTSVVYAEIK 142


```
QY 3 DIVVAAEYAPWSKTGGLGDTGGLPIELVKGRHVRMTIAPRY-----DOYADAWDTS 55
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
132 NIIFVTAEAAPSKTGGLGDSGLPVALAARGHRVWVSPRYLNGSPDEKYANAVDLD 191
QY 56 V--VVDIMG--EKVRFEHSIKKGVRHVRWIDHPFLAKVWCKTGSKLYGPRSGADYLDNHK 111
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
192 VRATVHCFGDAQVAYIHEYRAGVDWVFDVHSSYC-----RPGTP-YGDIYGA-FGDNQF 244
QY 112 RFALFCKAAEAARVLPFGP--GEDCVFVANDHWSALVPVLLKDEYQPKQFTKAKSVL 168
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
245 RETLLSHAACEAPLVPLSGFTYGEKCLFLANDHWAALVPLLLAAKYRPGVYKARSIV 304
QY 169 AHNIAFOGRWMEAEKDKLPQAAFDKLAISDGYAKVYVTEATPMEDEKPLPTGKTYKK 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
305 AHNIAHQGVPEAVTYNNLGLPPQWYGA---EWIPTWARHALD-----TGFT--- 351
QY 229 INWKGIIAADKLVTSPNYATEIAADAAGGVDELTVI--RAKGIEGLVNGMDIEWNP 286
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
352 VNVLKAIAVADRILLVSQYSWEIIT-PEGGYGLHELSSROSVLNGITNGIDVNDWNP 410
QY 287 KTDKFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFIFGRLEQKGVYDIIILAA 346
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
411 STDEHIAHYSINDL-SGKVOCKTDLQKELGLPIRPDCLPIGRLDYQKGVYDIIILSAI 469
QY 347 PKILATPKVQIAILGTGKAAEYKLVNAIGTKYKGRAGVVKTSAPLAHMLTAGADFMVLP 406
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
470 PELMQN-DVQVVMGSGEKOYEDWMRHTENLFDKFRWVGVNVPVSHRITAGCDILLMP 528
QY 407 SRFEPCGLIQLHAMHYGTVPVVASTGGLVDTVK-----EGV---TGFHMGALNPKDLD 456
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
529 SRFEPCGLNQLYAMRYGTPIVHSTGGLRDTYKDFNPYAGEGIGETGWTFSPLTSEKL- 587
QY 457 EADADALAATVRRASEVFAGGRYPE-----MVANCISODLSWSKPAQKWE 501
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
588 ---LDTPLKLA-----GTYTEHKSWSWEGLMRGMGRDYSWENAAIQYE 627

RESULT 8
US-09-192-909-2
; Sequence 2, Application US/09192909
; Patent No. 6307124
; GENERAL INFORMATION:
; APPLICANT: Jens Kossmann
; APPLICANT: Claus Froberg
; TITLE OF INVENTION: Nucleic acid molecules encoding soluble
; TITLE OF INVENTION: starch synthases from maize
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/192,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02527
; FILING DATE: 16-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 196 19 918.2
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, Jr., James F.
; REGISTRATION NUMBER: 27,794
```

```
; REFERENCE/DOCKET NUMBER: GFB-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-96-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 649 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-192-909-2

Query Match. 26.2%; Score 882.5; DB 4; Length 649;
Best Local Similarity 38.4%; Pred. No. 1.5e-68;
Matches 203; Conservative 95; Mismatches 174; Indels 57; Gaps 15;

QY 3 DIVVAAEYAPWSKTGGLGDTGGLPIELVKGRHVRMTIAPRY-----DOYADAWDTSV 56
Db 142 NIVFVTEASPYAKSGGLGDSGLPVALAARGHRVWVMPRYLNGTSDKNYANAFYTEK 201
QY 57 VVDIM---GE-KVRYFHSIKKGVRHVRWIDHPFLAKVWCKTGSKLYGPRSGADYLDNHKR 112
Db 202 HIRIPCGGHEVTFHEYRDSVDVWFVDHPSY-----HRPGLNGDKFEGA-FGDQFR 254
QY 113 FALFCKAAEAARVLPFGP--GEDCVFVANDHWSALVPVLLKDEYQPKQFTKAKSVLA 169
Db 255 YTLLCYAAACEAPLVPLSGFTYGEKCLFLANDHWAALVPLLLAAKYRPGVYKARSIV 314
QY 170 IHNIAFOGRWMEAEKDKLPQAAFDKLAISDGYAKVYVTEATPMEDEKPLPTGKTYKKI 229
Db 315 IHNIAHQGVPEASTYDGLLPPQWYGALEW-----VFPWARHRLDKG-----EAV 361
QY 230 NWLKGIIAADKLVTSPNYATEIAADAAGGVDELTVI--RAKGIEGLVNGMDIEWNP 287
Db 362 NELKGAVTADRIVTYKSGYSWEVTT-AEGQGLNELLSRKSVLNGIVNGIDINDWNP 420
QY 288 TDKFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFIFGRLEQKGVYDIIILAA 347
Db 421 TDKCIPCHYSVDDL-SGKAKCKGALQELGLPIRPDCLPIGRLDYQKGVYDIIILAI 479
QY 348 KILATPKVQIAILGTGKAAEYKLVNAIGTKYKGRAGVVKTSAPLAHMLTAGADFMVLP 407
Db 480 DLM-REDVQVVMGSGDPELEDWNRSTESIFDKFRGWSGVFVPSHRIITAGCDILMPS 538
QY 408 RFEPCGLIQLHAMHYGTVPVVASTGGLVDTVK-----EGVTFGHMGALNPKDLEA 458
Db 539 RFEPCGLNQLYAMRYGTPIVHSTGGLRDTYKDFNPYAGEGIGETGWTFSPLTSEKL- 594
QY 459 DADALAATVRRASEVFAGGR--YPEMVANCISODLSWSKPAQKWEGLLE 505
Db 595 ---MLWTPLKLAISTYREHKSWSWEGLMRGMGRDYSWENAAIQYE 639

RESULT 9
US-09-196-390-2
; Sequence 2, Application US/09196390
; Patent No. 6307125
; GENERAL INFORMATION:
; APPLICANT: Block, Martina
; APPLICANT: Lorz, Horst
; APPLICANT: Lutticke, Stephanie
; APPLICANT: Walter, Lennart
; APPLICANT: Froberg, Claus
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
; TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
```

COUNTRY: United States of America
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, V
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/196,390
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 196 21 588
 FILING DATE: 29-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 196 36 917
 FILING DATE: 11-SEP-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP97/02799
 FILING DATE: 28-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley, Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: AGRVO-9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 671 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-196-390-2

Query Match	26.1%	Score 881:	DB 4:	Length 671:
Best Local Similarity	35.2%	Pred. No. 2.2e-68;		
Matches 237; Conservative	94;	Mismatches 225;	Indels 118;	Gaps 22;
QY	4	IVMAAEVAPWSKTGGLGDVTGGLPTIELVKRGHRVMTIAPRY-----DQYADAWDTSVV	57	
Db	56	IYFVTGEAARYAKSGGLGDVCGSLPIALAARGHRVWVMPRYLNGSSDKNYAKALYAKH	115	
QY	58	VDIM-----GEKVRYFHSIKGVHRVWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHRF	113	
Db	116	IKIPCRGGSHVYFFHFHEYRDNDVDWVVDHP-----SYHRPGS-LYGDNFGA-FGDNQFRY	168	
QY	114	ALFCKAAIAAARVLPGP--GDCQFVANDWHSALVPVLLKDEYQKGOFTTRAKSVLAI	170	
Db	169	TLLCYAACAPLILELGGYTYGQCMFVNDWHSALVPVLLAKYRYGVYRUSRSLVLI	228	
QY	171	HNIAFOGRMEEAFKDTKLPOAADFCLAFSDGYAKVYTEATPMDEDEKPLTGKTYKIN	230	
Db	229	HNLAHQVEPASTYPLDGLPEWYGALEW-----VPEWARRHALDKG-----EAVN	275	
QY	231	WLKGGIIADKLVTVSPNATETATAAAGGVELDTVI--RAKGIEGLVGMDEEWNPKT	288	
Db	276	FLKGVAVTDRIIVTSQGYSEWETT-ABGQGLNELLSRKSRLVNGLVGIDINDWNPTT	334	
QY	289	DKFLSAPYDQNSVYAKAAKEALQAEGLGVPDPTAPLFAFIGLEBQKQGDITLALPK	348	
Db	335	DKCLPHYSVDDL-SCKAKCAEQLQELGLPVREDVPLIGFIRLDYKQGLIDLKMAIPE	393	
QY	349	ILATPKVQIALLGTGRAAYEKLNVNATGTYKGRAGVVKESAPLAHMLTAGADPMLVPSR	408	
Db	394	LM-REDVQFVYMLGSGDPIFEGWKRSTESSYKDKFRGWVGFVSPVSHRITAGCDILLMPSR	452	
QY	409	FEPCCGLTQLHAMHYGTVPVVASVGGGLVDIVK-----EGVTFGRMGALNPDKLDEAD	459	
Db	453	FEPCCGLNQLYAMQYGTVPVHVHGTGGLEDVTETENPFCAKEEGTGWAFSLPTVDKMLWA-	511	
QY	460	ADALATVRRASEVFGAGRPYEMVANCISODLSWSKPAQKVGALLLEEVYTKGGVATAKK	519	

```

Db      512  -----LRAMSTFRE-----HKPS--WEGLM-----KR 532
QY      520  EEIKVPAEKIPGDLPAVSYAPNTLKPVSASVEGNGAAAPKVGTWTAPMGAWRATTPSGP 579
Db      533  GMTKDHWDHAPSTSRSSSGPSWTNPTSC-----RRGLGRSKCEPSAL 577
QY      580  SPAAPAT--PKVTITYEPALPATAKPKTAGLK-LAGEASTTSTSENGAASNGNGNGASASK 635
Db      578  KTSSSRFRGPEGYPCITRCPATVESQCACLLWFAG-----SRTYDGCA-----AAAVT 625
QY      636  TSAAKPLVSAATR 649
Db      626  ASGGRQLQFWGIRK 639

RESULT 10
US-09-388-743-26
; Sequence 26, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ. ID. NO 26
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Typha latifolia
US-09-388-743-26

```

Query Match	25.9%	Score 873:	DB 4:	Length 801:
Best Local Similarity	38.9%	Pred. No. 1.5e-67:		
Matches 211: Conservative		Mismatches 166:	Indels 86:	Gaps 16:
QY	2	LDIVMVAEAPWSKGGLDGVTGGFLPIELVLRGHRVTMTAPYDQYADAWDTSV---VVD	59	
Db	226	MNIIVAAECAPWSKGGLDGVALPKALLARRGHRVAVPYGNYAEQPDIGVRKYK	285	
QY	60	IMGE--KVRYPHSIKKGVHRWIDHPFLAKVWCKTGSKLY-GRPSADYLDNHKRALF	116	
Db	286	VHQQDMEVTFYHAYIDGVDFVFMDSDFRHR-----GNRIYEGNR-----VDILKRMILF	335	
QY	117	CKAIIAARVLP-----FGPGECVCFVANDWHSAIVPVLKDEYQPKGQFTKAKSVLAH	171	
Db	336	CKAAEVPVHVPCGGFCYGDG-NLAFITNDWHHTALLEPYLKAYYRONGLMKYARSVLVIH	394	
QY	172	NIAFOGRMWEEAFKDKTLKPAQAFDKLAFSDGYAKVYTEATPMEDEKPIITGTYKKINW	231	
Db	395	NIAHQGRGVPDDKEFKVGLPHYLDLFRLYD-----PVGQ---EHLNI	433	
QY	232	LKGILTAADKLIVTSPNYATFELAADAGGVELDTVIRAKG--LEGIWNGMDIEWNEPKTD	289	
Db	434	FAAGLTKADRVTVTSHGYAWELKT--SEGGMGLHEIITNESWKQFGIVNGIDAKWSEFDD	492	
QY	290	KFTSAP----YDQNSVYVGAAKAAKEALQAEGLGFPVDPATLFAFIGLEBQKGVDIITLAA	345	
Db	493	VHLKSDGYTNYSLDTLEMGKPVCKAALQREVLGPVRDNPVLIATFIGRLDHQKGVDLIAEA	552	
QY	346	LPKILATPKVQIATLGTGKAAYEKLVNAIGTKYKRAKGVYKVSAPLAHMLTAGADEMLV	405	
Db	553	MPRIIV-SHDQYQVVLGVTGRODLENLRFNEFQHRDKVRWAVFVSQWRAHRTITAGADIIMM	611	
QY	406	PSRFEPGLQLHAMHYGTVPVVASTGGLVDIVTKEGVTGFHMGALNPDKLDEADADALAA	465	
Db	612	PSRFEPGLNQLYAMMYGTIPVHVHVGSLRDTVTQ-----FDPFNESSLGW	657	
QY	466	TVRRASEVFAGGRYPPEMWANCIS-----QDLWSKPKQKWEGILLEEV	507	

Db 51 IVFVTEASPYAKSGGLGDCVCSLPVLAALAAARGHRVMMVMPRYLNGTSDKNYANAFYTEKH 110
QY 58 VDIM---GE-KVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHKRF 113
Db 111 IRIPCFGGEHEVTFHEYRDSVDWVFDHPSY-----HRPGLNYGDKFGA-FGDNQFRI 163
QY 114 ALFCAAIAEAARVLPFGP---GDCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLAI 170
Db 164 TLCCYAAACEAPLLELGGYIYGONCMFVYNDWHSALVPVLLAAKYPYGVYKDSRLVI 223
QY 171 HNIAGQGRWEAFKDTKLPOAFAFKLAFSDGYAKVYVTEATPMEDEKPLTGKTYKKIN 230
Db 224 HNLHQGVPEPASTYDGLGLPPEWYGALEW-----VPEWARHRLDKG-----EAVN 270
QY 231 WLKGGIIAADKLVTVSPNVAETIAADAAGSVELDTVI--RAKIGIEGVNGMDIEENPKT 288
Db 271 FLKGAVVTADRIVTIVSKGYSWEVTT-AEGGQGLNELLSRKSVLNGVINGIDINDWNPAT 329
QY 289 DKFLSAPYDONSYYAKAAAEKALQAEGLPVDPTAPLFAFAGRLGEEQKGVDTIILAAKPK 348
Db 330 DKCIPCHYSVDL-SGKAKCKGALQKELGLPIRPDVLPIGFIGRLDYQKGDILQIIPD 388
QY 349 ILATPKVQIATLGTGKAAEKLVAIKTYKGRAGVVKFSAPLAHMLTAGADFMVPSR 408
Db 389 LM-REDVQVFMVLSGDPDEDMRSTESIFKDKFRGWGFSVPVSHRITAGCDILMPSR 447
QY 409 FEPCGLIOLHAMHYGTVPVVASTGGLVDTVK-----EGVTFGHMGAALNPKDL 455
Db 448 FEPCGLNQLYAMQYGVTVVHATGGLRDIVENFPFGENGEGQGTGNAFAPLTIENM 503

RESULT 13

US-08-941-445A-13
; Sequence 13, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P.
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-941-445A-13

Query Match 25.6%; Score 861.5; DB 3; Length 583;
Best Local Similarity 40.8%; Pred. No. 8.9e-67;
Matches 194; Conservative 81; Mismatches 154; Indels 47; Gaps 13;
QY 4 IVVMAAEVAPWSKTGGLGVDVTGGLPIELVKRHRVMTIAPRY-----DOYADAWDTSVV 57
Db 95 IVFVTEASPYAKSGGLGDCVCSLPVLAALAAARGHRVMMVMPRYLNGTSDKNYANAFYTEKH 154
QY 58 VDIM---GE-KVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHKRF 113
Db 155 IRIPCFGGEHEVTFHEYRDSVDWVFDHPSY-----HRPGLNYGDKFGA-FGDNQFRI 207
QY 114 ALFCAAIAEAARVLPFGP---GDCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLAI 170
Db 208 TLCCYAAACEAPLLELGGYIYGONCMFVYNDWHSALVPVLLAAKYPYGVYKDSRLVI 267
QY 171 HNIAGQGRWEAFKDTKLPOAFAFKLAFSDGYAKVYVTEATPMEDEKPLTGKTYKKIN 230
Db 268 HNLHQGVPEPASTYDGLGLPPEWYGALEW-----VPEWARHRLDKG-----EAVN 314
QY 231 WLKGGIIAADKLVTVSPNVAETIAADAAGSVELDTVI--RAKIGIEGVNGMDIEENPKT 288
Db 315 FLKGAVVTADRIVTIVSKGYSWEVTT-AEGGQGLNELLSRKSVLNGVINGIDINDWNPAT 373
QY 289 DKFLSAPYDONSYYAKAAAEKALQAEGLPVDPTAPLFAFAGRLGEEQKGVDTIILAAKPK 348
Db 374 DKCIPCHYSVDL-SGKAKCKGALQKELGLPIRPDVLPIGFIGRLDYQKGDILQIIPD 432
QY 349 ILATPKVQIATLGTGKAAEKLVAIKTYKGRAGVVKFSAPLAHMLTAGADFMVPSR 408
Db 433 LM-REDVQVFMVLSGDPDEDMRSTESIFKDKFRGWGFSVPVSHRITAGCDILMPSR 491
QY 409 FEPCGLIOLHAMHYGTVPVVASTGGLVDTVK-----EGVTFGHMGAALNPKDL 455
Db 492 FEPCGLNQLYAMQYGVTVVHATGGLRDIVENFPFGENGEGQGTGNAFAPLTIENM 547

RESULT 14

US-09-388-743-6
; Sequence 6, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthesis Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6

; LENGTH: 690
; TYPE: PRT
; ORGANISM: Curcuma zedoaria
US-09-388-743-6

Query Match 25.5%; Score 858; DB 4; Length 690;
Best Local Similarity 39.0%; Pred. No. 2.4e-66;
Matches 208; Conservative 80; Mismatches 176; Indels 70; Gaps 15;
QY 2 LDIVMAAEVAPWSKTGGLGVDVTGGLPIELVKRHRVMTIAPRYDOYADAWDTSVV---- 57
Db 199 MNILVAAECAPWSKTGGLGVDVVGALPKALAKRHRVMMVSPRYGPEPKEIGNLKRYK 258
QY 58 VDIMGEKVRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHKRFALFC 117
Db 259 VDGQDMEIKYHYTIDSVDFVFDSP-----IFRHGNDIY----GKNRVDIILKMWLFC 309
QY 118 KAAIEAARVLP-----FGPCDVCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLAHN 172
Db 310 KAAVEYPWHVPCGFCYGDG-NLVFIANDWHTSLLPVYLKACFDRCLMTYARCLLVHN 368

QY 173 IAFQGRMWEAFKDTKLPOAFAFDKLAFLSDGYAKVYTEATPMEDEKPPITGKTYKKINWL 232
Db 369 IAHQGRGLDFDYVDLHIDHSFLDD-----PVGGEHF-----NIF 407
QY 233 KGGIIAADKLTVSPNYATEIAADAAGGVLDTVIRA--KGIEGVNGMDIEEWNPKTDK 290
Db 408 AAGIRAADRVTVSHGYAWELKT-SEGWGLHEIINECHKWPHGVINGIDHSHWPKFDA 466
QY 291 FLSAP-----YDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFVIGLEEQKGVDTIILAA 346
Db 467 HLNSDGYNTLETLEMGKACQKAAALQREFGLPVRDDVPILLAFVIGRLDHQKGDILIAEAM 526
QY 347 PKILATPKVOIALIGTGKAAEYKLYNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVLP 406
Db 527 -HWLWQDQLIMUGTGRPDLEMLRREFEREHRGKVRGWGVFSVKMAHRTITAGADALLMP 585
QY 407 SRFEPCGLIQLHAMHYGTVPVVASTGGVLDTVKE-----GVTFGHMGALNPDKLEADADA 462
Db 586 SRFEPCGLNQLHAMMYGIPIVHVAYGGLRDTVQOQDFDPNEIGLW-----TFDRAEHR 539
QY 463 LAA-----TVRRASEVFAGRYPEMVANCISQDLSWSKPAQKWEGLLEEVVY 509
Db 640 MIVALGHCLNTYRNYKESWGLQKRGMM-----QDLSWESAHEYKVLVAAKY 688

RESULT 15
US-08-836-567-6
; Sequence 6, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 558 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-836-567-6

Query Match 25.1%; Score 845; DB 4; Length 558;
Best Local Similarity 39.1%; Pred. No. 2.3e-65;
Matches 207; Conservative 78; Mismatches 184; Indels 60; Gaps 14;
QY 2 LDIVVAAEVAWPSWTKGGLGVDVGGTGLPIELVVRGHRVMTIAPRYDOYADAMDTSV-----V 57
Db 67 MNIIIVASRCAPSWTKGGLGVAGALPKALARHRVMTVAPRYDNPPEQDSGVKKIYK 126
QY 58 VDIMGEKVRYPHSIKKGHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKKRALFC 117
Db 127 VDGQDVEVYFOAFIDGVDFVID-----SHMERHIGNNIY-----GGRNRVDILKRWLF 177
QY 118 KAAIEAARVLP-----FGGEDCVFVANDWHGALVPLVKDEYQPKGQFTKAKSVLAHN 172
Db 178 KAAIEVPWHPVPCGGVCYGDG-NLVFIANDWHHTALLPVYLKAYYRONGIMNYTRSVLVIHN 236
QY 173 IAFQGRMWEAFKDTKLPOAFAFDKLAFLSDGYAKVYTEATPMEDEKPPITGKTYKKINWL 232
Db 237 IAHQGRGLDFDYVDLPHYMDPFKLYD-----PVGGEHF-----NIF 275
QY 233 KGGIIAADKLTVSPNYATEIAADAAGGVLDTVIRA--KGIEGVNGMDIEEWNPKTDK 290
Db 276 AAGLKADRVTVSHGYAWELKT-SOGWGLHGIINENDWKLGIVNGIDTRENPELDV 334
QY 291 FLSAP-----YDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFVIGLEEQKGVDTIILAA 346
Db 335 HLQSDGYMNYSLDTLTQTKGPKCAALQKELGLPVRDDVPILLAFVIGRLDHQKGDILIAEAS 394
QY 347 PKILATPKVOIALIGTGKAAEYKLYNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVLP 406
Db 395 ANMMG-QDVQLVNLGTGRDLEQLRQFECQHNDKIRGWGVFSVKTSHRTITAGADILLMP 453
QY 407 SRFEPCGLIQLHAMHYGTVPVVASTGGVLDTVKE-----GVTFGHMGALNPDKLEADADA 460
Db 454 SRFEALRLNQLYAMKYGIPIVHVAYGGLRDTVQOQDFDPNEIGLW-----TFDRAEHR 513
QY 461 DALAATVRRASEVFAGRYPEMVANCISQDLSWSKPAQKWEGLLEEVVY 509
Db 514 NCL-LTYREYKKSWEG-----IQTRCMTQDLSWDAQAQNYEEVLIAAKY 556

Search completed: June 4, 2003, 14:58:35
Job time : 16.5821 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:56:21 ; Search time 20.1047 Seconds
(without alignments)
3342.965 Million cell updates/sec

Title: US-09-980-771a-3_COPY_58_708
Perfect score: 3370
Sequence: 1 ALDIVMAAEVAPWSKTGL.....SASKTSAAKPLVSAATRKSA 651

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues
Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1450.5	43.0	636	9 US-10-138-075-4	Sequence 4, Appli
2	1433.5	42.5	609	9 US-10-138-075-2	Sequence 2, Appli
3	1379	40.9	599	9 US-10-138-075-5	Sequence 5, Appli
4	881	26.1	671	10 US-09-952-677-2	Sequence 2, Appli
5	841	25.0	799	10 US-09-952-677-6	Sequence 6, Appli
6	555	16.5	915	9 US-10-163-214-6	Sequence 12, Appli
7	549	16.3	914	9 US-10-163-214-12	Sequence 2, Appli
8	545	16.2	909	9 US-10-163-214-2	Sequence 13, Appli
9	537	15.9	874	9 US-10-163-214-13	Sequence 99, Appli
10	410.5	12.2	474	12 US-10-007-693-99	Sequence 69, Appli
11	402.5	11.9	476	12 US-10-007-693-69	Sequence 10, Appli
12	385.5	11.4	293	9 US-10-163-214-10	Sequence 2, Appli
13	215.5	6.4	117	10 US-09-739-438-2	Sequence 4738, Ap
14	206	6.1	409	9 US-09-738-626-4738	Sequence 5896, Ap
15	189	5.6	381	9 US-09-738-626-5896	Sequence 4, Appli
16	164	4.9	143	10 US-09-739-438-4	Sequence 22, Appli
17	155.5	4.6	191	10 US-09-924-358-22	Sequence 3951, Ap
18	155.5	4.6	418	9 US-09-738-626-3951	Sequence 18, Appli
19	136.5	4.1	385	10 US-09-767-041-18	

20	135	4.0	2993	9 US-09-738-626-6239	Sequence 6239, Ap
21	134.5	4.0	1222	10 US-09-137-531-15	Sequence 15, Appli
22	134.5	4.0	1252	10 US-09-137-531-9	Sequence 9, Appli
23	129	3.8	1125	9 US-10-100-957A-152	Sequence 152, Appli
24	129	3.8	1610	9 US-10-100-957A-22	Sequence 22, Appli
25	128	3.8	2910	9 US-10-124-800-2	Sequence 2, Appli
26	126	3.7	387	9 US-09-738-626-3890	Sequence 3890, Ap
27	125.5	3.7	398	10 US-09-934-899-16	Sequence 16, Appli
28	125.5	3.7	398	10 US-09-934-899-36	Sequence 36, Appli
29	124.5	3.7	1704	9 US-09-991-262-40	Sequence 40, Appli
30	124	3.7	379	9 US-09-738-626-6655	Sequence 6655, Ap
31	124	3.7	1461	9 US-10-021-955-88	Sequence 88, Appli
32	123.5	3.7	413	9 US-09-738-626-4025	Sequence 4025, Ap
33	123	3.6	1528	9 US-09-945-917-3	Sequence 3, Appli
34	123	3.6	1583	9 US-09-945-917-4	Sequence 4, Appli
35	121	3.6	339	9 US-09-847-208-116	Sequence 116, Appli
36	118.5	3.5	372	10 US-09-815-242-5277	Sequence 5277, Ap
37	118.5	3.5	384	10 US-09-815-242-12605	Sequence 12605, A
38	118	3.5	267	10 US-09-852-555-2	Sequence 2, Appli
39	118	3.5	333	9 US-09-847-208-147	Sequence 147, Appli
40	118	3.5	1463	9 US-09-971-536-69	Sequence 69, Appli
41	117.5	3.5	636	9 US-09-738-626-5590	Sequence 5590, Ap
42	117	3.5	3241	10 US-09-841-786-1	Sequence 1, Appli
43	117	3.5	3739	9 US-09-860-846-33	Sequence 33, Appli
44	117	3.5	3739	9 US-09-988-384B-33	Sequence 33, Appli
45	117	3.5	3739	9 US-09-836-821-33	Sequence 33, Appli

ALIGNMENTS

RESULT 1

US-10-138-075-4
; Sequence 4, Application US/10138075
; Publication No. US20030087369A1
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Orozco, Emil M.
; TITLE OF INVENTION: Granule-Bound Starch Synthase
; FILE REFERENCE: BB1474 NA
; CURRENT APPLICATION NUMBER: US/10/138,075
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/288,315
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Glycine max
US-10-138-075-4

Query Match	43.0%	Score	1450.5;	DB	9;	Length	636;
Best Local Similarity	53.0%	Pred. No.	6.2e-95;				
Matches	291;	Conservative	71;	Mismatches	144;	Indels	43;
Gaps	10;						
QY	2	LDIVMAAEVAPWSKTGLGVDVTGGTGLPTELKRGHVMVIAPIRYDQYADAWDTSVVVDI-	60				
Db	106	MFFIIIGTEVAPWCVTGGGLGDLGPPALAGFGHVMVITVPRYDQYKDAWDTSVVIEVK	165				
QY	61	---MGEKRYFHISIKKGVHVMIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHKRFALFC	117				
Db	166	VCDRTKRYFHCYKRGVDVDFVDFHPWFLKVGKTGKLYGPTTGNEDYNQLRSLFC	225				
QY	118	KAIEAARVLPF-----GP-GEDEVFANDWHSALVPVLLKDFYQPKGFQAKSVIA	169				
Db	226	QAALAPRVLSNLSKSYFSGPYGDEVFVANDWHTALIPCYLKSMSYQSGIYTNARVFC	285				
QY	170	IHTIAFCQRMWEAEAFKDKLPQAADFKAFLSDGYAKVYTEAIPEMEDEKPPITGTYKKI	229				

```

Db 286 IHNIAYOGRFAFADFSLNLPDQKSSDFIDGHVK-----PVVG---RKI 328
QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGGVELDTVIRA-----KGIEGVNGMDIEWN 285
Db 329 NWLKGIIAADKLVTVSPNYATEIAADAAGGVELDTVIRA-----KGIEGVNGMDIEWN 388
QY 286 PKTDFLSAPYDONSUYAGKAAAEALQAEGLPVDPTAPLFAFAGRLLEEQKGVDIILAA 345
Db 389 PTTDKYIAKYDVSVLEAKALLKEALQAEGLPVDNRNPLIFIGFGRLEEQKGSILAEA 448
QY 346 LPKILATEKVQIAILGTCTKAAAYEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFMV 405
Db 449 IPQFT-KONVOLVALGTCKKOMEKOLELEISYDPKARGVAKFNVPFLAHMIIAGADFILV 507
QY 406 PSRFPCCGLIQLHAMHYGTPVPAVASTGGGLVDVFKGVTFGHMGNALNP--DKLDEADADA 463
Db 508 PSRFPCCGLIQLQAMRYGSPVIVASTGGGLVDVFKGVTFGHMGNALNP--DKLDEADADA 567
QY 464 AATVRRASEVFAGGRYPENVANCISQDLSWSKPAOKWEGLLBEVYV-----GKGG--VAT 516
Db 568 SKTVRALAVYGTAFTEIKNKMAQDLSWKGPAAKEWBEVLLSLGVPGSGDGEETAP 627
QY 517 AKKEEIKVP 525
Db 628 QAKENVATP 636

RESULT 2
US-10-138-075-2
; Sequence 2, Application US/10138075
; Publication No. US20030087369A1
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Orozco, Emil M.
; TITLE OF INVENTION: Granule-Bound Starch Synthase
; FILE REFERENCE: BB1474 NA
; CURRENT APPLICATION NUMBER: US/10/138,075
; PRIOR FILING DATE: 2002-05-02
; CURRENT FILING DATE: 2002-05-02
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Zea mays
US-10-138-075-2

```

```

Query Match 42.5%; Score 1433.5; DB 9; Length 609;
Best Local Similarity 52.3%; Pred. No. 9.4e-94;
Matches 288; Conservative 75; Mismatches 139; Indels 49; Gaps 11;

QY 2 LDIVMVAEAVAPWSKTGGIGDVTGGLPIELVKRGHRVMTIAPRYDOYADAWDTSVVYDI- 60
Db 81 MTIVFVATEVHPWCKTGGIGDVTGGLPIELVKRGHRVMTIAPRYDOYADAWDTSVLVEV 140
QY 61 MG---EKVYFHSIKKGVHRVMTIDHPWFLAKYWGKGTGSKLYGPRSGADYLDNKKRFA 117
Db 141 IGDVTETVFFHCYKRGVDRVFDHPWFLAKYWGKGTGSKLYGPRSGADYLDNKKRFA 200
QY 118 KAAIEAARVLFP-----GP-CEDCVFVANDWHSALVPLVKDEYQPKGQFTKAKSVLA 169
Db 201 LAALAPRVNLNNSSEYFSGPVGVANDWHTAILPCYLKSMVKPNKGIYVNAKAVPC 260
QY 170 IHNIAPQGRMWEAEAKDKLPQAAFDKLAESDGYAKVYTEATPMEDEKPPPTGTGTYKKI 229
Db 261 IHNIAYOGRFAFADFSLNLPDQKSSDFIDGHVK-----PVVG---RKI 303
QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGGVELDTVIRA-----GKGG--VAT 288

```

```

Db 304 NNMKAGIIESDLVLTVSPHYVKELTSGDPKGVDELGVLRTPLEIGIVNGMDVYEDPST 363
QY 289 DKFLSAPYDONSUYAGKAAAEALQAEGLPVDPTAPLFAFAGRLLEEQKGVDIILAA 348
Db 364 DKYISAKYDATTVTARALNKERLQAEGLPVDSSITPVIIVFGRLEEQKGSILIAAIFE 423
QY 349 ILATPKVQIAILGTCTKAAAYEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFMV 408
Db 424 FVG-ENVQIIVLGTGKKMEELTQLEVKYPPNARGIAKFNVPFLAHMIFAGADFIIVPSR 482
QY 409 FPCCGLIQLHAMHYGTPVPAVASTGGGLVDVFKGVTFGHMGNALNP--DKLDEADADA 466
Db 483 FPCCGLIQLQGRYGVIPICSSITGGGLVDVFKGVTFGHMGNALNP--DKLDEADADA 542
QY 467 VRRASEVFAGGRYPENVANCISQDLSWSKPAOKWEGLLBEVYVKGK-----GV 514
Db 543 VTRALKQYDTPAFHEMVQNCMAQDLSWKGPAAKW-----EVLGLGVESGRAGIDDAEEI 598
QY 515 ATAKEEIKVP 525
Db 599 APLAKENVATP 609

RESULT 3
US-10-138-075-5
; Sequence 5, Application US/10138075
; Publication No. US20030087369A1
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Orozco, Emil M.
; TITLE OF INVENTION: Granule-Bound Starch Synthase
; FILE REFERENCE: BB1474 NA
; CURRENT APPLICATION NUMBER: US/10/138,075
; PRIOR FILING DATE: 2002-05-02
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-138-075-5

```

```

Query Match 40.9%; Score 1379; DB 9; Length 599;
Best Local Similarity 50.4%; Pred. No. 6.8e-90;
Matches 277; Conservative 78; Mismatches 147; Indels 48; Gaps 10;

QY 2 LDIVMVAEAVAPWSKTGGIGDVTGGLPIELVKRGHRVMTIAPRYDOYADAWDTSVVYDI 61
Db 72 MPILFVATEVHPWCKTGGIGDVTGGLPIELVKRGHRVMTIAPRYDOYADAWDTSVVYDI 131
QY 62 ----GKVFYFHSIKKGVHRVMTIDHPWFLAKYWGKGTGSKLYGPRSGADYLDNKKRFA 117
Db 132 VGRDTEVTFVFFHCYKRGVDRVFDHPWFLAKYWGKGTGSKLYGPRSGADYLDNKKRFA 191
QY 118 KAAIEAARVLFP-----GP-CEDCVFVANDWHSALVPLVKDEYQPKGQFTKAKSVLA 169
Db 192 LAALAPRVNLNNSSEYFSGPVGVANDWHTAILPCYLKSMVKPNKGIYVNAKAVPC 251
QY 170 IHNIAPQGRMWEAEAKDKLPQAAFDKLAESDGYAKVYTEATPMEDEKPPPTGTGTYKKI 229
Db 252 IHNIAYOGRFPRVDFELLNPESFDFDVGHV-----PVVG---RKI 294
QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGGVELDTVIRA-----GKGG--VAT 288
Db 295 NNMKAGIIESDLVLTVSPHYVKELTSGDPKGVDELGVLRTPLEIGIVNGMDVYEDPST 354
QY 289 DKFLSAPYDONSUYAGKAAAEALQAEGLPVDPTAPLFAFAGRLLEEQKGVDIILAA 348

```

Db 355 DKVISYKYNATTVAERALKNEILQAEVGLPVDSSIPVIVFGRLEQKSGDILIAIPE 414
QY 349 ILATPKVQIAITLGTGAAYEKIVNAITGTYKGRAGKGVVKSAPLAHMLTAGADFMIVPSR 408
Db 415 FL-EENVQIIVLGTGKKMEELMELKAKYPQNGARTAKENVPLAHMFPAGANFIIIVPSR 473
QY 409 FEPGGLIQLHAMHYGTVPVVASTGGGLVDVTKEGVTGFHMGALNP--DKLDEADADALAT 466
Db 474 FEPGGLIQLGMYGIVIPICSSSTGGGLVDVTSEGVTFGHMGFSNFVEFIVDPADVAASN 533
QY 467 VRRASEVFFAGGRYPENVANCISODLSWSKPAQKWEGLLEEVVYKGG-----GVA 515
Db 534 VTRALQXKTPSPHANVQNCMAQDLSWKGPAKW-----EALILGLGVEGSGQGIIEEIA 589
QY 516 TAKKEIKVP 525
Db 590 PLAKQNVATP 599

RESULT 4

US-09-952-677-2
; Sequence 2, Application US/09952677
; Patent No. US20020138876A1
; GENERAL INFORMATION:
; APPLICANT: Block, Martina
; Lorz, Horst
; Luticke, Stephanie
; Walter, Lennart
; Froberg, Claus
; Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
; FROM WHEAT WHICH ARE INVOLVED IN STARCH
; SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,677
FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/196,390
FILING DATE: 19-NOV-98
APPLICATION NUMBER: DE 196 21 588.9
FILING DATE: 29-MAY-1996
APPLICATION NUMBER: DE 196 36 917.7
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: PCT/EP97/02793
FILING DATE: 28-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 671 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-952-677-2

Query Match 26.1%; Score 881; DB 10; Length 671;
Best Local Similarity 35.2%; Pred. No. 1.9e-54;
Matches 237; Conservative 94; Mismatches 225; Indels 118; Gaps 22;
QY 4 IVWVAARVAPWSKTGGGLGDTGGLPIELVKRGRHVMTIAPRY-----DOYADAWDTSVV 57
Db 56 IVEVTGEAPYAKSGGLGDCGSLPIALAARGHRVVMVMPRYLNGSSDKNYAKALYAKH 115
QY 58 VDIM----GEKVYFHSIKKGVHVVWDHFWLAKVWCKSKLYGPRSGADYLDNHRF 113
Db 116 IKTPCGSGSEVTFHEYRONVDMVFDHP-----SYHREGS-LYGNFNGA-FGDNQF 168
QY 114 ALFCKAAIEAARVLPFGP---GEDCVFVANDWHSALVPVLLKDYQPKGQFTAKSVIAI 170
Db 169 TLLCYAAACEAPLILELGGYIYGQNCMFVVDWHSALVPVLLAARYRYGVYVRSRSLVI 228
QY 171 HNIATFQGRWEEAFKDTKLPOAAFDKLAFGSDGAKVYVTEATPMEDDEKPLLTGTYKKIN 230
Db 229 HNLAHQGVPEASTYDGLPPEWYGALEW-----VPEWARHAKDKG-----EAVN 275
QY 231 WLKGGIITADKLVTVSPNYATEIAADAAGGVVELDTVI--RAKGGIEGVNGMDIEEWPKT 288
Db 276 FLKGVNADRIIVTSOGYSWEVTT-AEGGQGLNELLSRKSVLNGVINGIDINDWPTT 334
QY 289 DKFLSAPYDQNSYAGKAAAKEALQAEGLPVDPTAPLFAFVIGRLEEKQGVDIILAAAPK 348
Db 335 DKCLPHYSVDDL-SGKAKCKAELOKELGLPVREDVPLIGFVIGRLDYQKIDILKMAIPE 393
QY 349 ILATPKVQIAITLGTGAAYEKIVNAITGTYKGRAGKGVVKSAPLAHMLTAGADFMIVPSR 408
Db 394 LM-REDVQVYMLGSGDPIFEGWNRSTESSYKDKERGVWGSFVPSVSHRITAGCDILLMP 452
QY 409 FEPGGLIQLHAMHYGTVPVVASTGGGLVDTVK-----EGVTGPHMGALNPKLDEAD 459
Db 453 FEPGGLNQLXAMQYGVVPHVGGTGLDVTETNPFCAGKEEGTGWAFSLPTVDKMLWA- 511
QY 460 ADALATVRRASEVFFAGGRYPENVANCISODLSWSKPAQKWEGLLEEVVYKGGVATPAK 519
Db 512 -----LRTAMSTFRE-----HKPS--WEGLM-----KR 532
QY 520 EEIKVPVAEKIPGDLFAVSYAPNTLKPVSASVEGNGAAAPKVGTTPAMGAWRATTPSGP 579
Db 533 GMTKHTWDHAPSTSRSSSGPSWTNPTSC-----RGLGRKCESPSAL 577
QY 580 SPAAT---PKVTYTPALPATAKPKTAGLK-LAGEASTTSTSENGAASNGNGNGASAK 635
Db 578 KTSSSSFRGPEGYPCILRCPATVESQCACLLWFAG-----SRTYDCCA-----AAAVT 625
QY 636 TSAAKPLVSAATRK 649
Db 626 ASGGRQLQFWGIRK 639

RESULT 5

US-09-952-677-6
; Sequence 6, Application US/09952677
; Patent No. US20020138876A1
; GENERAL INFORMATION:
; APPLICANT: Block, Martina
; Lorz, Horst
; Luticke, Stephanie
; Walter, Lennart
; Froberg, Claus
; Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
; FROM WHEAT WHICH ARE INVOLVED IN STARCH
; SYNTHESIS

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:

DISK READABLE FORM.
MEDIUM TYPE: Floppy disk

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn R

ENT APPLICATION DATA:

APPLICATION NUMBER: US/0

FILING DATE: 14-Sep-2011

FILING DATE: 14-Sep-2001
R APPLICATION DATA.

FOR APPLICATION DATA:

APPLICATION NUMBER: 004105 200

APPLICATION NUMBER: 09/196,390

FILING DATE: 19-NO. US2002

APPLICATION NUMBER: DE 196 21 588.9

FILING DATE: 29-MAY-1996

APPLICATION NUMBER: DE 196 36 917.

FILING DATE: 11-SEP-1996

FILING DATE: 11 SEP-19
APPLICATION NUMBER: PC

APPLICATION NUMBER: PCT/EP
 FILING DATE: 29-MAY-1997

FILING DATE: 28-MAY-1997

RNEY/AGENT INFORMATION:

NAME: Haley, Jr., James F.

REGISTRATION NUMBER: 27,799

REFERENCE/DOCKET NUMBER: A

REFERENCE/DOCKING INFORMATION

TELECOMMUNICATION INFORMATION
FIFTH EDITION, 1973 506

TELEPHONE: (212) 596-9000

TELEFAX: (212) 593-1111

ON FOR SEQ ID NO:

ENCE CHARACTERIST

LENGTH: 799 amino acids

Ε

```

;
;      ILEU, AMINO ACID
;
;      TOPOLOGY: linear
;
;      MOLECULE TYPE: protein
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
US-09-952-677-6

```

```

Db      752  ALGHCL-RTYEDPKE-----SWRALQERGSQDFSEWEHAAKLYEDVLVKAKY  797

RESULT 6
US-10-163-214-6
; Sequence 6, Application US/10163214
; Publication No. US20030097688A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-163-214-6

```

US-10-163-214-12
 ; Sequence 12, Application US/10163214
 ; Publication No. US20030097688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Stephen M.
 ; APPLICANT: Broglie, Karen E.
 ; APPLICANT: Butler, Karlene H.
 ; APPLICANT: Thorpe, Catherine J.
 ; TITLE OF INVENTION: Starch Synthase Isoform V
 ; FILE REFERENCE: BB1520 US NA
 ; CURRENT APPLICATION NUMBER: US/10/163,214
 ; CURRENT FILING DATE: 2002-06-05
 ; PRIOR APPLICATION NUMBER: 60/297,099
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 12
 ; LENGTH: 914
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 US-10-163-214-12

Query Match 16.3%; Score 549; DB 9; Length 914;
 Best Local Similarity 30.8%; Pred. No. 1.1e-30;
 Matches 169; Conservative 89; Mismatches 202; Indels 88; Gaps 22;

QY	2	LDIVMVAEAPWSKTGGLGVDVTGGLPTIELVKRGHVMITAPRYD-QYADAWDTSVVVDI	60
Db	421	LHIHIAEAPVAKVGLADVISGLKALQKKGHLVEILLPKYDCMQVDQVSNLKVLVD	480
QY	61	MGEKRYFHSIKKGVRHVMIDHPWFLAKVWGT--GSKLY--GPR-----SGADYLDN	110
Db	481	LVQS--YF-----EGMNFNKKIWTGTEGLPVYFIEPOHPAMFFSRAQYGEH	526
QY	111	---KRFALFCKAAIEAARVLPFGCEDC-VFVANDWHSALVPVLKDEYQKQFTKAS	166
Db	527	DDFKRFSYFSAALE-----LLYQSGKKVDIIHCHDWQTAFAVAPLYWDVYANLG-FNSARI	581
QY	167	VLATHNIAFOGRMWEAFKDTKLPOAEDKLAFLSDGYAKVYTEATPMEDEKPP-LTKGT	225
Db	582	CFTCHNFEYQG-----TAPARDLAWC-----GLDVEHLDRPDRMRDNS	619
QY	226	YKINLWKGGLIAADKLVTSVSNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEWN	285
Db	620	HGRINAVGAVVSNIVTTSPTVALEVRSEGGRLQDTLKVHRSKFLGILNGIDTDTWN	679
QY	286	PKDKFSLAPYDQNSVYAGKAAKEALQAEGL-PVDPPTAPLFAFGRLEOKGVDIILAA	344
Db	680	PCTDRYLKVOYSNADKL-OGKAANKAALREQLNLASAYPSQPLVGCITRLVAQKGVHLIRH	738
QY	345	ALPKILATPKVQIAITLGTGKAAYEKLVAIGTKYKGRA-----KGVVKFSAPLAHM	395
Db	739	AIYK-TAELGGQFVLLGSSP-----VPEIQREFEGADHFQNNNNIKLIILYDDALSHC	791
QY	396	LTAGADEMLVSRPEPCGLIQLHAMHYGTVPVASTGGGLVDV---KEGVTGFHMGALN	451
Db	792	IYAASDMFVPSIPEPCGLIQMIAMRYGSYPIVRKGTGLNSVDFDEDTIP---MEVRN	848
QY	452	PKDLDEADALATVRRASEVFRAGGYPPEMVANCISODL-----SNKSPAKKWGLLEE	507
Db	849	GFTTVKADQGLSSAMERAFNCYT--RKPEVWKOLVQKDMTIDFSWDTASQYEDIYQKA	906
QY	508	VYKGGVA 515	
Db	907	VARAVA 914	

RESULT 8
 US-10-163-214-2
 ; Sequence 2, Application US/10163214
 ; Publication No. US20030097688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Stephen M.

; APPLICANT: Broglie, Karen E.
 ; APPLICANT: Butler, Karlene H.
 ; APPLICANT: Thorpe, Catherine J.
 ; TITLE OF INVENTION: Starch Synthase Isoform V
 ; FILE REFERENCE: BB1520 US NA
 ; CURRENT APPLICATION NUMBER: US/10/163,214
 ; CURRENT FILING DATE: 2002-06-05
 ; PRIOR APPLICATION NUMBER: 60/297,099
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 2
 ; LENGTH: 909
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 US-10-163-214-2

Query Match 16.2%; Score 545; DB 9; Length 909;
 Best Local Similarity 29.4%; Pred. No. 2.1e-30;
 Matches 159; Conservative 92; Mismatches 199; Indels 90; Gaps 20;

QY	2	LDIVMVAEAPWSKTGGLGVDVTGGLPTIELVKRGHVMITAPRYD-QYADAWDTSVVVDI	60
Db	416	LHIHIAEAPVAKVGLADVISGLKALQKKGHLVEILLPKYDCMQHQNINNLKVLVD	475
QY	61	MGEKRYFHSIKKGVRHVMIDHPWFLAKVWGT--GSKLY--GPRSGADYL-----	107
Db	476	-----VVKSYFEGNMFANKIWTGTEGLPVYFIEPOHPGKFFWRAQYGEH	521
QY	108	DNHKEFALFCKAAIEAARVLPFGCEDC-VFVANDWHSALVPVLKDEYQKQFTKAS	166
Db	522	DDFKRFSYFSALE-----LLYQSGKKVDIIHCHDWQTAFAVAPLYWDVYANLG-FNSARI	576
QY	167	VLATHNIAFOGRMWEAFKDTKLPOAEDKLAFLSDGYAKVYTEATPMEDEKPP-LTKGT	226
Db	577	CFTCHNFEYQG-----TAPADQLAYCGLDVHDLRDPDR--MRDNSH	615
QY	227	KKINLWKGGLIAADKLVTSVSNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEWN	286
Db	616	GRINAVGAVVSNIVTTSPTVALEVRSEGGRLQDTLKVHRSKFLGILNGIDTDTWN	675
QY	287	KDKFSLAPYDQNSVYAGKAAKEALQAEGL-PVDPPTAPLFAFGRLEOKGVDIILAA	345
Db	676	STDRFLKVOYSANDYL-GKSANKAALRKOLKLASTQASQPLVGCITRLVPOKGVHLIRH	734
QY	346	LPKILATPKVQIAITLGTGKAAYEKLVAIGTKYK--GRKGVVKSAPLAHMLTAGADF	402
Db	735	IVKITELGG-OPVLLGSSPVQHIQREFEGADHFQNNNNVRLLLKYDDALAHMIFAASDM	793
QY	403	MLVPSRPEPCGLIQLHAMHYGTVPVASTGGGLVDV-----VKEGVTGFHMGAL	450
Db	794	FIVPSMFEPCGLITQMVAMRYGSVPVVRTGTGLNSVDFDDEDTIPMEVRNGFTFL----	848
QY	451	NPDKLDEADALATVRRASEVFRAGGYPPEMVANCISODL-----SNKSPAKKWGLLEE	506
Db	849	---KADEQD---FGNALERAFNY--HRKPEVWKOLVQKDMKIDFSWDTSVSQQYEETQK	900

RESULT 9
 US-10-163-214-13
 ; Sequence 13, Application US/10163214
 ; Publication No. US20030097688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Stephen M.
 ; APPLICANT: Broglie, Karen E.
 ; APPLICANT: Butler, Karlene H.
 ; APPLICANT: Thorpe, Catherine J.
 ; TITLE OF INVENTION: Starch Synthase Isoform V
 ; FILE REFERENCE: BB1520 US NA
 ; CURRENT APPLICATION NUMBER: US/10/163,214
 ; CURRENT FILING DATE: 2002-06-05
 ; PRIOR APPLICATION NUMBER: 60/297,099
 ; PRIOR FILING DATE: 2001-06-08

```

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 874
; TYPE: PR1
; ORGANISM: Vigna unguiculata
US-10-163-214-13

```

Query Match	15.9%	Score 537;	DB 9;	Length 874;
Best local similarity	30.4%;	Pred. No. 7.5e-30;		
Matches 168;	Conservative	85;	Mismatches 191;	Indels 108; Gaps 25;
QY	2	LDIVMAAEVAPWSKTGGGLDVTGGPIELVKKGRHVMTIAPRYD--QYADAWDTSVVVD	59	
DB	377	LYVHIAAEAMAPVAKVGGGLDVSIGLSKALQKKGHLVEIILPKYDCMQYDRIGDLR-ALD	435	
QY	60	IMGEKVVYHSIKKGVHVMIDHPWLAKVMGKT--GSKLY-----GPRSQA	104	
DB	436	VWIES--YF-----DCQLFNKNIWGTVEGLPVFTFEPHPGKFFWNGDYIGA	481	
QY	105	DYLDNKHKRALFCAAIEAARVLFPFGGEDCVFVANDHWSALVPLVLKDEYQPKGQFTKA	164	
DB	482	H--DDFRFYSFRAALEF--LLQAGKKPDIH-CHDQTAFTAPLYWDVYAPKG-LNSA	535	
QY	165	KSVLATHNTIAFOGWMEEAEFKOTKLQAAFDKLAFSQYAKVYTEATPEMEDEKPLPTGK	224	
DB	536	RICFTCHNFPYQGTAGASELEAGLDSHQINR-----PDMQDN-----S	575	
QY	225	TYKKNLWKGIIAACKLVTVSPNYATEIAADAGGVELDTVI--RAKGIEGIVNGMDIE	282	
DB	576	AHRNRSVKGAVVYSNIVTVSTYTAQEVST-APGGKGLHSTLSTHSKKFTIGLNGIDTD	634	
QY	283	ENWPKTDKPLSAPVDNSVYAGAAAKEALQAEGL-LPVDPTAPLFAFIGLEQKGVDI	341	
DB	635	IWPATDPTFLQVQYANDL-QGKSENKEALRRNLGLSSADVRRPLVGCILFLVPQGVHL	693	
QY	342	ILAAFLKILATPKV-QIALGTGCKAAEYKLVNAGTKYKGRA-----KGVKQFSA	390	
DB	694	IRHA--YYITLDELGGFVLLGSSPVPH-----IQREFEGIANHFNQDHIRLILKYDE	744	
QY	391	PLAHMLTAGADEMLVSRFEPGGLIQLHAMHYGTPVVAVSTGGLVDVY-----	438	
DB	745	SLSHAIYAASDMFTIIPSEFPCGLTQMLSMRYGAIPARTKGTGLNDVSFVDVDDDTIPSQF	804	
QY	439	KEGVTGFHMGALNPKDLDEADADALAAATVFRASEVTFAGG--RYEMFYANCISQDLSWKP	496	
DB	805	RNGFT-----FLNAD--EKGINDALV---RAINLFTNDPKSWKOLQKMDNIDFSWSS	853	
QY	497	AQKWEGILLEVVY	508	
DB	854	AAOYEELYSKSV	865	

RESULT 10
US-10-007-693-99
; Sequence 99, Application US/10007693
; Patent No. US20020146776A1

APPLICANT: Bhatia, Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.515C2
CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 157

```

; SEQ ID NO 99
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis serovar D
US-10-007-693-99

```

Query Match

```

Best Local Similarity 28.2%; Pred.No. 3.1e-21;
Matches 148; Conservative 72; Mismatches 206; Indels 99; Gaps 22;

QY      2 LDIVMAAEVAPKSGGLGDDVTGGLEFIELVKRGHRVMTIAPRYOYADAWDTSVVVDIM 61
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MKIIHTAIEFAPVIKAGGLGDALYGL-AKALAAANHTEVVIPLYPKLFTLPKREQDLCSI- 58

QY      62 GEKVRFP-----HSIKKGVHRVTDHPWFLAKVWGKTSGLYKPRSGADYL 107
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      59 -QKLSYFFAGEQFATAFSYFEGIKVTLFKL-----DFOPELFENAEITYS 104

QY      108 DNHKRALFCKAAI-----EAARVLPFGPEGECVFVANDWHSALVPVLLKDEYQPKQFT 162
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      105 DDAFRCAFSAAASYYIQEGANIVHL-----HDWHTGLVAGLLKQ--QPCSQLQ 152

QY      163 KAKSVTAIHNIAFGRMWEBAFQDKLPQANFKLAFSDGYAKVYEAATPMEDEKPLLT 222
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      153 KI--VLTLLHNGFYRGVYTTREILEASSLINE-----FYISQVQLFRDPQTCVL 196

QY      223 GKTYKKINWLKGGTIAADKLIVTSPNYATEIFAADAAGGVELDTVIRAK--GIEGIVNGMD 280
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      197 -----LKGALYCSDFVTVTSPTYAKEILEDYS-DYEIHDAITARQHHLRGILLNGID 246

QY      281 IEFWNPKTDKFLSAPYDQ-----NSVYAGAAKAEALQAEGLVPDTPAPLFAFTGRLE 334
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      247 TTIWGPETDNLAKNTKELFTPTSFIFEAKENKKALYERLGLSLE-HSPCCWCIISRIA 305

QY      335 EQKGVDIILALPKILATPKVQIAITGL--GKAAYEKLVN---AIGTKYKGRKGVVVKFS 389
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      306 EQKGPHEMKQAILHALENAYTLI-LIGTCYGNQLHEEFANLQESLANSPPVRI--LLTYS 362

QY      390 APIAHMLTAGADPMLVPSREPCGLIQLHAMHVGTVPPVASTGGLDVTYKEGVTHGMGA 449
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      363 DVLARQIFAAADMICIPSMFEPGCLTOMIGFYGTPLVRATGLADTVANGINGFSF--420

QY      450 LNP-DKLDEADADALATVRASGAVRAGGYEPMVNCI--SODL 491
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      421 FNPDDFYEFNMLSEAVTYYTNRH----DNKQHLIVRACLDFFSDDL 461

RESULT 11
US-10-007-693-69
; Sequence 69, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007,693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 69
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-10-007-693-69

```

Query Match	11.9%	Score 402.5	DB 12	Length 476
Best Local Similarity	26.9%	Pred. No. 1.2e-20		
Matches 150	Conservative 78	Mismatches 204	Indels 125	Gaps 24
Qy	4	IVVAAEVPWSKTGGGLDVTGGPIELVKRGHVTIAPRY---	DOYADAWDTSVVVDI	60
Db	3	IVQVAVEFTPIVKVGGLDGAVASLSKELAQ-NDVEVLLPHYPLISKSS-		54
Qy	61	MGEKVRVTHSIKKGVHVRWIDHPWFLAKVWGCTGSKLYGP-		105
Db	55	LSERSFYE-----	FLGKQCAISAISYSEYGLTLITITLDSQIELFTSTV	99
Qy	106	YLDNH-KRFALFCKAAIEAARVLPFGGEGDCVFVANDWHSALVPVLLKDFQPKGQTKA		164

Db 100 YSENNVVFSAFAAAA--AAVLQADPAD--IVHLHDWHVCLLAGLLKNPLN-----VHS 151
QY 165 KSVLAIHNIHQHWEAKDKLPQAAFDKLAFLSDGYAKVYTEATPMEDEKPLTGK 224
Db 152 KIVFTIHNFYRG-----YCSYQLLAAS-----QIDDFHLSHY-----QLFRDPQTSV 194
QY 225 TYKKINWLGKGIITAAADKLVTSPNYATEIAADAAGGVLELDTVIRAKG--IEGIVNGMDIE 282
Db 195 L-----MKGALVCSYDITVSLTYVQEIINDYS--DYELHDAILARNSVFGILINGIDE 247
QY 283 ENWPKTKFISAPYD-----QNSVYAGKAAAEALQAEGLPVDPTAPLFAFGRLEEQ 336
Db 248 VWNPKTDPALAVQVDSILLSEPDVLTFTKEENRAVLVEKLGISSD-YFPLICVLSRIVEE 306
QY 337 KG-----VDIILAALPKILATPKVQIATLGTGKAAAYEKLVAIGKYKGRAG-----VVK 387
Db 307 KGPEFMKEIILHAMEHSYA-----FILGTSQ-----NEVLLNEFRNLQDCLASSPNIRLILD 359
QY 388 FSAPLAHMLTAGADFMVPSREFPCGLIQLHAMHYGTPVVPVASTGGGLVDTVKGVGTGFHM 447
Db 360 FNDPLARTYAADMICIPSHREACGLTQLIAMRYGIVPLVRKTGGGLADIVPGVNGFTF 419
QY 448 GALNPKLDEADADALAATVRRASEVFAGGRYPFEMVANCISODLSWSKPAQKWGLLEEV 507
Db 420 --EDTNFNE-----FRAMLSNAV-----TYRQEPDVLNLLIESG 453
QY 508 VYCKGGVATAKKEIKV 524
Db 454 MLRASGLDAMAKHYVNL 470

RESULT 12

US-10-163-214-10
; Sequence 10, Application US/10163214
; Publication No. US20030097688A1

GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-163-214-10

Query Match 11.4%; Score 385.5; DB 9; Length 293;
Best Local Similarity 33.0%; Pred. No. 9.5e-20;
Matches 101; Conservative 59; Mismatches 115; Indels 31; Gaps 9;
QY 228 KINWLGKGIITAAADKLVTSPNYATEIAADAAGGVLELDTVIRAKGIEGIVNGMDIEWNP 287
Db 1 RINAVKGAVVYNIIVTSPYALEVRSRGRGLQDTLKVHRSKFLGILNGIDTDWNP 60
QY 288 TDKFISAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFGRLEQKGVDTIILAL 346
Db 61 TDYKLVQYNKDL--OGKAANKAAALREQLNASYPSQLVGCITRLVAQKGVHLIRHAI 119
QY 347 PKILATPKVQIATLGTGKAAAYEKLVAIGKYKGR-----KGVVKESAPLAHMLT 397
Db 120 YK-TAELGQFVLLGSSP-----VPEIQREGEIADHFQNNNNIRLILKYDDALSHCIY 172
QY 398 AGADFMVPSREFPCGLIQLHAMHYGTPVVPVASTGGGLVDTV-----KEGVTGFHMGALNPD 453
Db 173 AASDMFIVPSIEPCGLTQMIAMRYGSPVIVRKTGGLNDSVDFEDDETIP---MEVRNGF 229

QY 454 KLDEADADALAATVRRASEVFAGGRYPFEMVANCISODL-----SWSKPAQKWGLLEEVY 509
Db 230 TFVRADEGLSSAMERAFNCYT--RKPEVWKQLVQKMDTIDFSDWTSASQIEDIYOKAVA 287
QY 510 GKGVVA 515
Db 288 RARAVA 293

RESULT 13

US-09-739-438-2

; Sequence 2, Application US/09739438

; Patent No. US20020029394A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Beckles, Diane M.

; APPLICANT: Thorpe, Cathy

; TITLE OF INVENTION: Homologs of Starch Synthase DUI

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/739,438

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: 60/171514

; PRIOR FILING DATE: 1999-12-22

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 2

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Oryza sativa

US-09-739-438-2

Query Match

Best Local Similarity 6.4%; Score 215.5; DB 10; Length 117;

Matches 41; Conservative 17; Mismatches 25; Indels 5; Gaps 1;

QY 356 QIALGTG-----KAAYEKLVAIGTKYKGRAGKGVKFSAPLAHMLTAGADFMVPSRFE 410
Db 8 QVVLGSA PDHRIQGDFTNLASKLHGEYHGRVKLCITYDEPLSHLIYAGADFILVPSMFE 67
QY 411 PCGLIQLHAMHYGTPVVPVASTGGGLVDTV 438
Db 68 PCGLTQLTAMRYGSIPIVRKTGGGLYDTV 95

RESULT 14

US-09-738-626-4738

; Sequence 4738, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI

; APPLICANT: MIZOGUCHI, HIROSHI

; APPLICANT: ANDO, SEIKO

; APPLICANT: HAYASHI, MIKIRO

; APPLICANT: OCHIALI, KEIKO

; APPLICANT: YOKOI, HARUHIKO

; APPLICANT: TATEISHI, NAKO

; APPLICANT: SENOH, AKIHIRO

; APPLICANT: IKEDA, MASATO

; APPLICANT: OZAKI, AKIO

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: JP 99/377484

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: JP 00/159162

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: JP 00/280988

; NUMBER OF SEQ ID NOS: 7059

; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 4738

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 08:28:25 ; Search time 3394.54 Seconds
(without alignments)
16743.883 Million cell updates/sec

Title: US-09-980-771A-4

Perfect score: 1953

Sequence: 1 gcgcgtgacatcgtgatggt.....ccgcaccgcgaagtcgcgc 1953

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1953	100.0	1953	6	AX049325	Sequence
2	1953	100.0	2124	6	AX049323	Sequence
3	1953	100.0	3117	6	AX049322	Sequence
4	1951.4	99.9	3240	8	AF026420	Chlamydom
5	1953	81.6	1593	6	AX049329	Sequence
6	1314	67.3	1314	6	AX049327	Sequence
7	962.2	49.3	5856	8	AF433156	Chlamydom
8	536.8	27.5	2289	8	AF286320	Triticum
9	530	27.1	1812	8	AF486514	Hordeum v
10	530	27.1	2311	8	HVWAXYR	Hordeum v
11	528.4	27.1	1827	8	AF486515	Hordeum v
12	528.4	27.1	1827	8	AF486518	Hordeum v
13	525.6	26.9	2127	8	AF163319	Triticum
14	525.2	26.9	1812	8	AF486519	Hordeum v
15	525.2	26.9	1827	8	AF486516	Hordeum v
16	525.2	26.9	1827	8	AF486517	Hordeum v
17	524	26.8	1605	8	AF250137	Triticum
18	505.4	25.9	2028	8	AF113844	Triticum
19	505.2	25.9	2186	8	TAWAXYSS	Wheat waxy
20	505.2	25.9	2267	8	AY050174	Triticum
21	481.4	24.6	1801	8	AF113843	Triticum
22	475.8	24.4	2267	6	AK195560	Sequence
23	473.2	24.2	2115	8	AB089141	Setaria i
24	453.6	23.2	2287	8	SBU23945	Sorghum bic
25	449	23.0	1937	8	AB066093	Oryza sat
26	449	23.0	1937	8	AB066094	Oryza sat
27	447.4	22.9	2542	6	AB106491	Sequence
28	447.4	22.9	2542	8	GSWX	X74160 M.esculenta
29	347	17.8	2168	8	MEGBSS	Phaseolus
30	340.2	17.4	2270	8	AF210699	Ipomoea b
31	329.6	16.9	2221	8	AB029546	Sequence
32	321.6	16.5	2211	8	AB071604	Chlamydom
33	316.8	16.2	2161	6	AX394246	Ipomoea b
34	313.2	16.0	2345	8	AMA6293	Sequence
35	312.8	16.0	3049	8	AF026421	Antirrhin
36	305.6	15.6	2124	8	IBU44126	Ipomoea bat
37	298	15.3	2092	8	AY094405	Arabidops
38	298	15.3	2115	8	AY088544	Arabidops
39	298	15.3	2192	8	AY123983	Arabidops
40	289.5	14.8	2107	8	AF097922	Astragalu
41	283.2	14.5	764	8	AF446083	Miscanthu
42	279.6	14.3	2035	8	PSSTARSYN	P.sativum m
43	274.2	14.0	2081	8	AF109395	Triticum
44	274	14.0	764	8	AF446082	Microsteg
45	273.2	14.0	721	8	AF446081	Cleistach

ALIGNMENTS

RESULT 1
LOCUS AX049325
DEFINITION Sequence 4 from Patent WO0071734.
ACCESSION AX049325
VERSION AX049325.1 GI:12226092
KEYWORDS
SOURCE synthetic construct.
ORGANISM
REFERENCE 1 (bases 1 to 1953)
AUTHORS D'Hulst,C. and Ball,S.
TITLE Starch granules containing a recombinant polypeptide of interest,
method for obtaining same and uses
JOURNAL Patent: WO 0071734-A 4 30-NOV-2000.

FEATURES
source

CDS

1.1953
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="fragment de l'ADN complet codant la GBSST de Chlamydomonas reinhardtii et codant la proteine GBSST mature"
/c1. >1953
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC21781.1"
/db_xref="GI:12226093"
/translation="ALDIIVMAAEVAPMSKGLGLDVTGGGLPIELVKRHRVMTIAPR
YDQYADNDSVVDIMGEKVPYFHSIKKGVHRVMDHPFLAKVKGKTSKLYGPRS
GADYLDNRKALFALCAALEARALPFGEDCVFVANDMHSALVPVLLKDEYQPKGQ
FTKAKSLAHNIAFOGRWEEAFDKLPQAFADKLPFADYKAYVITATPEWEEK
PPLTKYTKINLWKGIIADKLIVSPNAYATEIAAAGGVDELTVIRAKIGIV
NGMDTEENPKDKELSPADONSVAGKAKEALQAEGLPVPDTPAFLEFIGLE
EOKGVDIILALPKLILATPKVOIAILGTGKAAYEKLVNAIGTKYKRAKGVYKFSAPL
AHLJAGADEMLVPSRPPCGLIQLHAMHYGVNVPVASTGGLDVKEGVTGFHMGAL
NDPKLDEADALAIATVRRASEVFAAGRPYEMVANCISQDLSSWPAQKWEGLLEVV
YKGGVATAKKEEIKVPVAEKIPGDLPAVSYAPNFIKPVSAVEGNGAAAPKVGITAP
AMGAWRATTPSGPSAAATPKVTYKPALPATAPKPTAGLKLAGEASTTSTSENGAAS
NGNGNGASASKTSAAPKPLVSAATRKSA"

BASE COUNT 344 a 712 c 608 g 289 t

ORIGIN

Query Match 100.0%; Score 1953; DB 6; Length 1953;
Best local similarity 100.0%; Pred. No. 1e-184;
Matches 1953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGGACATCTGATGTTGCTGAGTGGCTGCGCCCTTGTCTCCAGAGCGGGCGCTG 60
DB 1 GCCTGGACATCTGATGTTGCTGAGTGGCTGCGCCCTTGTCTCCAGAGCGGGCGCTG 60

QY 61 GGGGATGTGACTGGTGGCTGCTATTTAGCTGGTCAAGCGCGGCCACCGCGTCATGACC 120
DB 61 GGGGATGTGACTGGTGGCTGCTATTTAGCTGGTCAAGCGCGGCCACCGCGTCATGACC 120

QY 121 ATGGCCCTCGTACGACAGTACGCTGACGCTGGGACACCTCGGTGGTCTGGGACATC 180
DB 121 ATGGCCCTCGTACGACAGTACGCTGACGCTGGGACACCTCGGTGGTCTGGGACATC 180

QY 181 ATGGCGGAGAGGTCGCTACTCCATCCATCAAGAGGCGGTGACCGCGTGTGATT 240
DB 181 ATGGCGGAGAGGTCGCTACTCCATCCATCAAGAGGCGGTGACCGCGTGTGATT 240

QY 241 GACCACCCCTGGTTCCTGGCCAAAGTCTGGGCAAGACCGGCTCCAAAGCTGTACGGCCCC 300
DB 241 GACCACCCCTGGTTCCTGGCCAAAGTCTGGGCAAGACCGGCTCCAAAGCTGTACGGCCCC 300

QY 301 CGCTCCGGCGCTGACTACCTGGGCAACCAAGCGCTTCGCCCTTCTGCAAGGCGCT 360
DB 301 CGCTCCGGCGCTGACTACCTGGGCAACCAAGCGCTTCGCCCTTCTGCAAGGCGCT 360

QY 361 ATTGAGGCTGCGCGCTGCTGCGCTTCGCGCGGAGGACTCGCTTCTGTCGCGCAAC 420
DB 361 ATTGAGGCTGCGCGCTGCTGCGCTTCGCGCGGAGGACTCGCTTCTGTCGCGCAAC 420

QY 421 GACTGGCACTCGCGCTTGGTGGCCGCTCTGCTGAAGGACGAGTACCGCCCAAGGGCCAG 480
DB 421 GACTGGCACTCGCGCTTGGTGGCCGCTCTGCTGAAGGACGAGTACCGCCCAAGGGCCAG 480

QY 481 TTCACCAAGGCAAGTGGTGGCTGGCTATCCACACATCGCTTCCAGGGCGCATG 540
DB 481 TTCACCAAGGCAAGTGGTGGCTGGCTATCCACACATCGCTTCCAGGGCGCATG 540

QY 541 GAGGAGGCTTTCAAGGACACGAGTGGCTGCGCGGAGGCGGCTTTGACAAAGCTTCTCG 600
DB 541 GAGGAGGCTTTCAAGGACACGAGTGGCTGCGCGGAGGCGGCTTTGACAAAGCTTCTCG 600

QY 601 GACGGTATGCCAAGGTTTACACTGAGGCCACCCCATTTGAGGAGGACGAGAGCCCGG 660
DB 601 GACGGTATGCCAAGGTTTACACTGAGGCCACCCCATTTGAGGAGGACGAGAGCCCGG 660

QY 661 CTGACGGGAAAGACTACAGAAGATCAACTGGCTGAAGGTTGGCATTATTCGCCGCCGAC 720
DB 661 CTGACGGGAAAGACTACAGAAGATCAACTGGCTGAAGGTTGGCATTATTCGCCGCCGAC 720

QY 721 AAGCTGTGACTGTGTGCGCCCAACTACGCGACCGAGATCGCTGCCGATGCGCGCGGT 780
DB 721 AAGCTGTGACTGTGTGCGCCCAACTACGCGACCGAGATCGCTGCCGATGCGCGCGGT 780

QY 781 GTGGAGCTGGACACCGTATCCGCGCAAGGGCATTTGAGGGCATTTGTAACGGCATGGAC 840
DB 781 GTGGAGCTGGACACCGTATCCGCGCAAGGGCATTTGAGGGCATTTGTAACGGCATGGAC 840

QY 841 ATTGAGAGTGGAAACCCCAAGACCGCAAGTTCCTGCTGCGCCCTACGACCAAGACAGC 900
DB 841 ATTGAGAGTGGAAACCCCAAGACCGCAAGTTCCTGCTGCGCCCTACGACCAAGACAGC 900

QY 901 GTCTAGCCCGGCAAGGCGCGCCCAAGAGGCGCTCGAGGCGCGCTGAGGCGCTGCTGTG 960
DB 901 GTCTAGCCCGGCAAGGCGCGCCCAAGAGGCGCTCGAGGCGCGCTGAGGCGCTGCTGTG 960

QY 961 GACCCACCGCCCTGTTGCTTTCATCGCGCGCTGAGGAGGAGAGGGTGTGAC 1020
DB 961 GACCCACCGCCCTGTTGCTTTCATCGCGCGCTGAGGAGGAGAGGGTGTGAC 1020

QY 1021 ATCATCTGCGCGCTGCGCCCAAGATCTGCGCCACCGCCCAAGGTGCAAGTGCCTGCTG 1080
DB 1021 ATCATCTGCGCGCTGCGCCCAAGATCTGCGCCACCGCCCAAGGTGCAAGTGCCTGCTG 1080

QY 1081 GGTACCGGCAAGGCGCGCTACGAGAAGTGTGTAAAGCGCATTCGCGCACCAAGAGGC 1140
DB 1081 GGTACCGGCAAGGCGCGCTACGAGAAGTGTGTAAAGCGCATTCGCGCACCAAGAGGC 1140

QY 1141 CGCGCCAAAGGCGGTGCTAAGTTCGCGCGCCCTCGCGCATGCTCACCGCGCGGCC 1200
DB 1141 CGCGCCAAAGGCGGTGCTAAGTTCGCGCGCCCTCGCGCATGCTCACCGCGCGGCC 1200

QY 1201 GACTTCATGCTGTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1260
DB 1201 GACTTCATGCTGTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1260

QY 1261 CACTACGCTACCGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1261 CACTACGCTACCGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

QY 1321 GCGGTACCGGCTTCCACATGGGCGCGCTGAAACCGCCGACAGCTGGAGAGGCTGACGCC 1380
DB 1321 GCGGTACCGGCTTCCACATGGGCGCGCTGAAACCGCCGACAGCTGGAGAGGCTGACGCC 1380

QY 1381 GACGCGCTTGGCGCCACCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1440
DB 1381 GACGCGCTTGGCGCCACCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1440

QY 1441 GAGATGTGGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 GAGATGTGGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500

QY 1501 GAGGCGCTGCTGAGGAGGCTGTGTACGGCAAGGCGCGCTGGCCACCGCCCAAGAGGAG 1560
DB 1501 GAGGCGCTGCTGAGGAGGCTGTGTACGGCAAGGCGCGCTGGCCACCGCCCAAGAGGAG 1560

QY 1561 GAGATCAAGTGTGCGGTTGCGGAGAGATCCCGCGCGACTTCCCGCGCGCTTCTCTACGCC 1620
DB 1561 GAGATCAAGTGTGCGGTTGCGGAGAGATCCCGCGCGACTTCCCGCGCGCTTCTCTACGCC 1620

QY 1621 CCCAACACCTTGAGGCGCGCTGCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 CCCAACACCTTGAGGCGCGCTGCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680

QY 1681 GTGCGCACCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740

```
|||||
Db 1681 GTGCGACACCGCCCGCCATGGCGCTGGCGCGGACACACCCCTCGGGCCCTCG 1740
QY 1741 CCGCGCGCGCCACCCGACAGGTGACACCTACAAAGCCGCGCTGCGCGGACCGCCCAAG 1800
Db 1741 CCGCGCGCGCGACCCGACAGGTGACACCTACAAAGCCGCGCTGCGCGGACCGCCCAAG 1800
QY 1801 CCCAAGACCGCTGGCTCAAGCTGGCGGTGAGGCTCCACACCTCGACCTCGGAGAAC 1860
Db 1801 CCCAAGACCGCTGGCTCAAGCTGGCGGTGAGGCTCCACACCTCGACCTCGGAGAAC 1860
QY 1861 GCGCTGCTCCAAAGCGCAACGGGCTGCTCGGCTCCAAAGACCTCGGCTGCCAAG 1920
Db 1861 GCGCTGCTCCAAAGCGCAACGGGCTGCTCGGCTCCAAAGACCTCGGCTGCCAAG 1920
QY 1921 CCCCTGCTCCCGCGCCACCGCAAGTCGCGC 1953
Db 1921 CCCCTGCTCCCGCGCCACCGCAAGTCGCGC 1953

RESULT 2
AX049323
LOCUS AX049323 2124 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 2 from Patent WO0071734.
ACCESSION AX049323
VERSION AX049323.1 GI:12226090
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE
AUTHORS 1 (bases 1 to 2124)
TITLE D'Hulst,C. and Ball,S.
JOURNAL Starch granules containing a recombinant polypeptide of interest,
Patent: WO 0071734-A 2 30-NOV-2000;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source
1. .2124
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/translation="fragment de la sequence compl te de l'DNAC codant
la gRSSI de Chlamydomonas reinhardtii."
1. .>2124
/note="unnamed protein product"
/codon_start=1
/translation="1"
/db_xref="GI:12226091"
/translation="MAVASTSRPSSARPPIVINAAGVYKKTANOLLRELARGSKST
SRSAVTGATGATCALDIVMAAEVAPWSTGGLGDTGGLPIELVYKRGHVRMTIAPRY
DOYADWTSVVVDIMGEKRVFHSIKKGVHRWIDHPWFLAKVWGTGSKLYGPRSG
ADYLDNHKREALFCKAAEAARVLFPFGEDCVFVANDWHSALVPLVLLKDEYOPKGF
TKAKSVLAHNTAFGRWMEAFKDTLPQAAFDKLAISDGYAKVYVTEATPMEDEKP
PLTGTYKINWLGIIIAADKLVTSPNATFIAADAAGVELDVIIRAKETIGLVN
GMIDIEWPNTDFTLSAPDQNSVYAGRAAAKEALQAEGLPVDPTAPLFAFIRLEE
QKGVDIILAAALPKIILATPKVOIILGTGAAYEKLVAIGTKYKGRAGVYKESAPLA
HMLTAGADFMVLPSPREPCGLIQLHAMHVGTPVVASGGLVDTVKEGTGFHMGALN
PDKLDEADALAAVTRASEVFAAGRPTEPMVANCISQDLWSKFAQKWEGLLEVVY
KGGVATRAKKEIKVPVAEKIPGDLPAVSYAPNTLKPSVASVEGGAAPKVGTTAPA
MGAWRATTPSGPSAAATPKVITYKPAALPATAKPTAGLKLAGEASTTSTSENGAASN
GNNGASASKTSAAPKPIVSAATRKA"
BASE COUNT 369 a 773 c 656 g 326 t
ORIGIN
Query Match 100.0%; Score 1953; DB 6; Length 2124;
Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 1953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGCTGGACATGCTGATGTTGCTGAGCTGAGCTGCGCCCTTGGTCCAAAGCGGCGCGCTG 60
Db 172 GCGCTGGACATGCTGATGTTGCTGAGCTGAGCTGCGCCCTTGGTCCAAAGCGGCGCGCTG 231
QY 61 GCGCATGTGACTGGTGGCTGCTATTGAGCTGGTCAAGCGCGGCGCACCGCGCTGATGACC 120
|||||
232 GSCGATGTGACTGGTGGCTGCTATTGAGCTGGTCAAGCGCGGCACCGCGCTCATGACC 291
QY 121 ATTGCCCTCGCTAGCACCAGTACGCTGACGCTGGGACACACCTCGGTGTGTGGACATC 180
Db 292 ATTGCCCTCGCTAGCACCAGTACGCTGACGCTGGGACACACCTCGGTGTGTGGACATC 351
QY 181 ATGGCGGAGAAAGTCCGCTACTTCCACTCCATCAAGAGGGGTGCACCGCTGTGGATT 240
Db 352 ATGGCGGAGAAAGTCCGCTACTTCCACTCCATCAAGAGGGGTGCACCGCTGTGGATT 411
QY 241 GACACACCTCGTGTCTGGCCAAAGGTCTGGGCAAGACCGGCTCCAAAGCTGTACGCGCCC 300
Db 412 GACACACCTCGTGTCTGGCCAAAGGTCTGGGCAAGACCGGCTCCAAAGCTGTACGCGCCC 471
QY 301 CGCTCCGCGCTGACTACTTCCGACACCAACGAGCCCTTCGCGCTTCTTCTGAAGCGCGCT 360
Db 472 CGCTCCGCGCTGACTACTTCCGACACCAACGAGCCCTTCGCGCTTCTTCTGAAGCGCGCT 531
QY 361 ATTGAGGCTGCCCGCTGCTGCCCTTCGCGCCCGCGGAGGACTGGCTCTTCTGTGGCCCAAC 420
Db 532 ATTGAGGCTGCCCGCTGCTGCCCTTCGCGCCCGCGGAGGACTGGCTCTTCTGTGGCCCAAC 591
QY 421 CACTGGGACTCCGCGCTGGTGGCGGTCTCTGTGAAGGACGAGTACGAGCCCAAGGGCCAG 480
Db 592 GACTGGGACTCCGCGCTGGTGGCGGTCTCTGTGAAGGACGAGTACGAGCCCAAGGGCCAG 651
QY 481 TTCACCAAGGCAAGTGGTGTGGCTATCCACACATCGGCTTCCAGGGCGCATGTGG 540
Db 652 TTCACCAAGGCAAGTGGTGTGGCTATCCACACATCGGCTTCCAGGGCGCATGTGG 711
QY 541 GAGGAGGCTTTCAAGGACACCAAGCTGCCCGAGCGCGCTTTTGACAAGCTGGCTTCTCG 600
Db 712 GAGGAGGCTTTCAAGGACACCAAGCTGCCCGAGCGCGCTTTTGACAAGCTGGCTTCTCG 771
QY 601 GACGGCTATGCAAGGTTTACACTGAGGCCACCCCGCATGAGGAGGACGAGAACCGCCCG 660
Db 772 GACGGCTATGCAAGGTTTACACTGAGGCCACCCCGCATGAGGAGGACGAGAACCGCCCG 831
QY 661 CTGACGGGAAGACCTACAAGAGTCAACTGGCTGAAGGGTGCATATATCGCGCGCGAC 720
Db 832 CTGACGGGAAGACCTACAAGAGTCAACTGGCTGAAGGGTGCATATATCGCGCGCGAC 891
QY 721 AAGCTGTGACTGTGTGCGCCCACTACGCGACCCGAGATCGCTGCCGATCGCGCGCGGT 780
Db 892 AAGCTGTGACTGTGTGCGCCCACTACGCGACCCGAGATCGCTGCCGATCGCGCGCGGT 951
QY 781 GTGAGCTGGACACCGCTATCCGCGCCCAAGGGCATTTGAGGCGCATTTGAAAGCGCATGAC 840
Db 952 GTGAGCTGGACACCGCTATCCGCGCCCAAGGGCATTTGAGGCGCATTTGAAAGCGCATGAC 1011
QY 841 ATTGAGGAGTGGAAACCCCAAGACCGACAAGTCTCTGTCTGCGCCCTACGACCAAGAC 900
Db 1012 ATTGAGGAGTGGAAACCCCAAGACCGACAAGTCTCTGTCTGCGCCCTACGACCAAGAC 1071
QY 901 GTCTACGCGCGCAAGGCGCGCCCAAGAGGCGCCTTCAGCGCGGAGTGGCGCTTCCCTGTG 960
Db 1072 GTCTACGCGCGCAAGGCGCGCCCAAGAGGCGCCTTCAGCGCGGAGTGGCGCTTCCCTGTG 1131
QY 961 GACCCACCGCCCGCTTGTTCGCTTTCATCGCGCGCGCTGGAGGACGAGAGGGTGTGGAC 1020
Db 1132 GACCCACCGCCCGCTTGTTCGCTTTCATCGCGCGCGCTGGAGGACGAGAGGGTGTGGAC 1191
QY 1021 ATCATCTGCGCGCGCTGCGCAAGATCTTGGCCACCCCGCAAGGTGCAGATCGCCATCTCTG 1080
Db 1192 ATCATCTGCGCGCGCTGCGCAAGATCTTGGCCACCCCGCAAGGTGCAGATCGCCATCTCTG 1251
QY 1081 GGTACCGGCAAGGCGCGCTTACGAGAAGCTGGTGAACCGCATCGGACCAAGTACAAGGCG 1140
Db 1252 GGTACCGGCAAGGCGCGCTTACGAGAAGCTGGTGAACCGCATCGGACCAAGTACAAGGCG 1311
QY 1141 CCGGCCAAGGGGTGTGTAAGTTCTCGCGCGCGCTTGGCGCACATGCTACCGCGCGCGC 1200
|||||
```


QY	961	GACCCACCGCCCGCCCTGTTCCGCTTCATCGCGCCCTGGAGGAGCAGAGGTTGTGCAC	1020
Db	1146	GACCCACCGCCCGCCCTGTTCCGCTTCATCGCGCCCTGGAGGAGCAGAGGTTGTGCAC	1205
QY	1021	ATCATCTGCGCGCCCTGCCAAGATCCTGGCCACCCCAAGTGCAGATGCCATCCTG	1080
Db	1206	ATCATCTGCGCGCCCTGCCAAGATCCTGGCCACCCCAAGTGCAGATGCCATCCTG	1265
QY	1081	GGTACCGGCAAGCGCCCTAGGAGAAGCTGTGAACGCTATCGACCAAGTACAAGGCG	1140
Db	1266	GGTACCGGCAAGCGCCCTAGGAGAAGCTGTGAACGCTATCGACCAAGTACAAGGCG	1325
QY	1141	CGCGCCCAAGGCGTGTCAAGTCTCGCGCCCTCGCGACATGCTCACCAGCGCGGCC	1200
Db	1326	CGCGCCCAAGGCGTGTCAAGTCTCGCGCCCTCGCGACATGCTCACCAGCGCGGCC	1385
QY	1201	GACTTCATGCTGTGCTCGCTCGCGCTTCGAGCCCTCGCGCTGATCCAGCTCAGCCCATG	1260
Db	1386	GACTTCATGCTGTGCTCGCTCGCGCTTCGAGCCCTCGCGCTGATCCAGCTCAGCCCATG	1445
QY	1261	CACCTACGGTACCGTGCCTGTGAGCTCCACCGCGCGCTGTGTCGACACCGTCAAGGAG	1320
Db	1446	CACCTACGGTACCGTGCCTGTGAGCTCCACCGCGCGCTGTGTCGACACCGTCAAGGAG	1505
QY	1321	GGCGTCAACCGCTTCCACATGGCGCCCTGAACCCCGACACAGCTGGAGGCTGACGCC	1380
Db	1506	GGCGTCAACCGCTTCCACATGGCGCCCTGAACCCCGACACAGCTGGAGGCTGACGCC	1565
QY	1381	GAGCGCCTGCGCCGACCGTGCCTGTGAGCGGCTGCTGAGCGGCTGTGTCGCGCGCGCTACGCC	1440
Db	1566	GAGCGCCTGCGCCGACCGTGCCTGTGAGCGGCTGCTGAGCGGCTGTGTCGCGCGCGCTACGCC	1625
QY	1441	GAGATGCTGCGCAACTGCATCAGCAGGACCTGTCTGTGTCGAGCGCGCCGCAAGTGG	1500
Db	1626	GAGATGCTGCGCAACTGCATCAGCAGGACCTGTCTGTGTCGAGCGCGCCGCAAGTGG	1685
QY	1501	GAGGGCTGCTGAGGAGGTGTGAGCGGCAAGGCGGCTGCTGAGCGGCTGTGTCGAGCGGCTACGCC	1560
Db	1686	GAGGGCTGCTGAGGAGGTGTGAGCGGCAAGGCGGCTGCTGAGCGGCTGTGTCGAGCGGCTACGCC	1745
QY	1561	GAGATCAAGGTGCGCTGTCGAGGAGATCCCGCGGACCTGCGCGCGCTGTCTACGCC	1620
Db	1746	GAGATCAAGGTGCGCTGTCGAGGAGATCCCGCGGACCTGCGCGCGCTGTCTACGCC	1805
QY	1621	CCCAACACCTGAAGCCCGTGTGCGCTCGTGGAGGCGCAAGCGCGCGCGCCGCGCAAG	1680
Db	1806	CCCAACACCTGAAGCCCGTGTGCGCTCGTGGAGGCGCAAGCGCGCGCGCCGCGCAAG	1865
QY	1681	GTCGGCACCAACCGCCCGCGCATGGCGCGTGGCGCGGACACCCCGCTCGGCGCGCTCG	1740
Db	1866	GTCGGCACCAACCGCCCGCGCATGGCGCGTGGCGCGGACACCCCGCTCGGCGCGCTCG	1925
QY	1741	CCGCGCGCGCGCACCGCCCGCAAGGTGACCTACAAGCGCGCGCTGCGCGCGCGCGCAAG	1800
Db	1926	CCGCGCGCGCGCACCGCCCGCAAGGTGACCTACAAGCGCGCGCTGCGCGCGCGCGCAAG	1985
QY	1801	CCCAAGACCGTGGCTCAAGCTGGCGGTGAGGCGCTCCACACCTCGACCTCGGAGAAC	1860
Db	1986	CCCAAGACCGTGGCTCAAGCTGGCGGTGAGGCGCTCCACACCTCGACCTCGGAGAAC	2045
QY	1861	GGCGCTGCCTTCCAAACGGCAACGGCAACGGTGTGCTGCGCGCTTCCAAAGACCTCGGCGT	1920
Db	2046	GGCGCTGCCTTCCAAACGGCAACGGCAACGGTGTGCTGCGCGCTTCCAAAGACCTCGGCGT	2105
QY	1921	CCCTGTGCTGCGCGCGCGCAAGTGCCTGCGCGCTTCCAAAGACCTCGGCGT	1953
Db	2106	CCCTGTGCTGCGCGCGCGCAAGTGCCTGCGCGCTTCCAAAGACCTCGGCGT	2138
RESULT 4			
AF026420			
LOCUS			

Chlamydomonas reinhardtii granule-bound starch synthase I precursor (STA2) mRNA, complete cds.

AF026420.3 GI:16716334

Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii.

Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonas.

1 (bases 1 to 3240)

D'Hulst,C., Wattedbled,F., Ral,J.-P., Abel,G.J., Kossmann,J. and Ball,S.G.

Cloning of a cDNA encoding for the GBSSI in the green alga Chlamydomonas reinhardtii

Unpublished

2 (bases 1 to 3240)

D'Hulst,C., Abel,G.J., Kossmann,J. and Ball,S.G.

Direct Submission

Submitted (23-SEP-1997) Genetique Microbienne, Lab. Chimie Biologique UMR111 CNRS, Univ. Sci. Tech. de Lille, Villeneuve d'Ascq Cedex 59655, France

3 (bases 1 to 3240)

D'Hulst,C., Wattedbled,F., Ral,J.-P., Abel,G.J., Kossmann,J. and Ball,S.G.

Direct Submission

Submitted (20-JUN-2000) Groupe de Glycobiologie des Protistes, Laboratoire de Chimie Biologique, UMR 8576 du CNRS, Universite des Sciences et Technologies de Lille, Villeneuve d'Ascq Cedex 59655, France

Sequence update by submitter

4 (bases 1 to 3240)

D'Hulst,C., Wattedbled,F., Ral,J.-P., Abel,G.J., Kossmann,J. and Ball,S.G.

Direct Submission

Submitted (05-NOV-2001) Groupe de Glycobiologie des Protistes, Laboratoire de Chimie Biologique, UMR 8576 du CNRS, Universite des Sciences et Technologies de Lille, Villeneuve d'Ascq Cedex 59655, France

Sequence update by submitter

On Nov 5, 2001 this sequence version replaced gi:8573759.

Location/Qualifiers

1. .3240

/organism="Chlamydomonas reinhardtii"

/strain="137C"

/db_xref="taxon:3055"

/clone="CD142"

1. .3240

/gene="STA2"

138. .2264

/gene="STA2"

/EC_number="2.4.1.21"

/function="ADP-Glucose:alpha-1,4-D-glucan-4-alpha-D-glucosyltransferase"

/note="GBSSI"

/codon_start=1

/product="granule-bound starch synthase I precursor"

/protein_id="AAC17969.3"

/db_xref="GI:16716335"

/translation="MAVASTSRPSSRPVINAAPFGVKKTANOLLRELARGSARKSTSRVATGATGATCALDIVMAEAPVAPSWKSTGGLDVGTGGLPIELVKRGHVMITAPRYDOYADWDTSVVDVIMGEKVRIFHSIKGVRHVRVIDHPWFLAKVNGKTSKLYGRPSGADYLDNHRDFALFCAAEARVLPFGPCDVFVANDHWSALVPLVLLKDEYQPKQFPTKSVLAIHNTAFGRMEEAFKDTKLPQAAPDLAFSDGAKVVTATPEDEKPTKGTYYKIKNLKGGIIAADKLVTSVPNATEIAADAAGGVELDVIIRAKIGETVNGMDIEWNPKTDKELSPVDONSIVAGKAAKEALQALGLPVDPTAPLPAFTIGLEEOKGVLDLLAALPKILATPKYQIALLGTGKAATEKLVNAIGTKYKRGKRGVKSAPLAHMLTAGDFMLVPSRFECGLIQLHAMHYGTVPVASTGGLVITKRGVTFGHMGLNPKLDEADADALAAATVRRASEVFAGRYEPVANCISQDLSWSKPAQKWEGLLEEVYKGVGATARKKEIKVPAEKIPCDLPAVSAPNTLKPVSASVEGNAAPKVGTTAPAMGAWRATTPSGPSAAATPKVTYKPAIPATAPKATAGLAGEASTTSTSENGAASNGNGASASAKTSAAKPLVSAATKSA"

transit_peptide 138. .308

/gene="STA2"

DEFINITION Sequence 8 from Patent WO0071734.
ACCESSION AX049329
VERSION AX049329.1 GI:12226096
KEYWORDS synthetic construct.
SOURCE artificial sequences.
ORGANISM 1 (bases 1 to 1593).
AUTHORS D'Hallst,C. and Ball,S.
TITLE Starch granules containing a recombinant polypeptide of interest,
method for obtaining same and uses
JOURNAL Patent: WO 0071734-A 8 30-NOV-2000;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..1593
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="fragment de l'DNAc complet codant la GBSSI de
Chlamydomonas reinhardtii"
CDS 1..>1593
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC21783.1"
/db_xref="GI:12226097"
/translation="ALDIYVMAEVAEVPWSKGGDVTGGPIELVKRHRVMTIAPR
YDQADAWDTSVVDIGEKVYRHSIKKGVHRVWIDHPFLAKVMKGTGSKLYGPRS
GADYLDNHRFALECKAIEARVLFPFGEDCVFVANDHSAIYVLLKDEYOPKQG
PFLAKVLAHNIATFQGRWMEAFKDKLPQAAEDKLFASDGYAKVYTFEATPMBEDEK
PTKSGYTKVTKLWIKGLIAADKLVTSPNVAIEADAAGSVELDTVIRAKGLEIV
NGMDIEWNPRTDKPLSAPYQNSVYAKAAKEALDAELGLPVDTPAPLFAFTGRLE
EOKGVDIILALPKILATPKVQIAILGTGKAAYEKLNAIGTKYGRKAGVYKFSAPL
AHMLTAGADFMVSRPEPCGLIQHAMHYGTVPVASTGGVLVDIVKRGVTFHMGAL
NPDKLEADALAAATVRRASEVFAGGRYPEWVANCTSDLSWSKPAQKWGLLEEVV
YKGKGVAATKEELIKVPAEKIP"
BASE COUNT 290 a 539 c 510 g 254 t
ORIGIN
Query Match 81.6%; Score 1593; DB 6; Length 1593;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 1593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGCTGGACATCGTGTCTGCTGAGGTGCGCCCTTGCTCCAAAGCGGCGGCGCTG 60
Db 1 GCGCTGGACATCGTGTCTGCTGAGGTGCGCCCTTGCTCCAAAGCGGCGGCGCTG 60
QY 61 GCGGATGTGACTGTGGGCTGCTGCTATTGAGCTGGTCAAGCGGCGGCGGCTGATGACC 120
Db 61 GCGGATGTGACTGTGGGCTGCTGCTATTGAGCTGGTCAAGCGGCGGCGGCTGATGACC 120
QY 121 ATTGCCCTCGGTACGACAGTACGCTGACGCTGGGACACCTCGGTGCTGTGGACATC 180
Db 121 ATTGCCCTCGGTACGACAGTACGCTGACGCTGGGACACCTCGGTGCTGTGGACATC 180
QY 181 ATGGCGGAGAGTCCGTACTTCCACTCCATCAAGAGAGGGGCTGCACCGCTGTGGATT 240
Db 181 ATGGCGGAGAGTCCGTACTTCCACTCCATCAAGAGAGGGGCTGCACCGCTGTGGATT 240
QY 241 GACCAACCCCTGGTTCCTGGCCAAAGTCTTGGGCAAGACCGGCTCCAAAGTGTACGCGCCC 300
Db 241 GACCAACCCCTGGTTCCTGGCCAAAGTCTTGGGCAAGACCGGCTCCAAAGTGTACGCGCCC 300
QY 301 CGCTCCGGGCTGACTACTTGGCAACACACAGCGCTTCGCCCTGTCTGTGAAGGCGGT 360
Db 301 CGCTCCGGGCTGACTACTTGGCAACACACAGCGCTTCGCCCTGTCTGTGAAGGCGGT 360
QY 361 ATTGAGGTGCGCGCTGCTGCGCTTCGCGCCCGCGGAGAGTGGTCTCTGCTGGCCAC 420
Db 361 ATTGAGGTGCGCGCTGCTGCGCTTCGCGCCCGCGGAGAGTGGTCTCTGCTGGCCAC 420
QY 421 GACTGGCACTCGCGCTGCTGGTGGCCCGCTCTGCTGAAGAGGAGTACAGCCCAAGGCGCAG 480
Db 421 GACTGGCACTCGCGCTGCTGGTGGCCCGCTCTGCTGAAGAGGAGTACAGCCCAAGGCGCAG 480

QY 481 TTCACCAAGGCCAAGTCGGTGGCTATCCACAAATCGCTTCCAGGGCCGATGTGG 540
Db 481 TTCACCAAGGCCAAGTCGGTGGCTATCCACAAATCGCTTCCAGGGCCGATGTGG 540
QY 541 GAGGAGGCTTTCAAGGACACGAAAGTGCGCCAGGCGCCCTTTCACAAAGTGTGGCTTCTCG 600
Db 541 GAGGAGGCTTTCAAGGACACGAAAGTGCGCCAGGCGCCCTTTCACAAAGTGTGGCTTCTCG 600
QY 601 GAGGCTATGCCAAGGTTTACACTGAGGGCCACCCCATGAGGAGGACGAGAGGCCCCCG 660
Db 601 GAGGCTATGCCAAGGTTTACACTGAGGGCCACCCCATGAGGAGGACGAGAGGCCCCCG 660
QY 661 CTGACGGGAAGACCTACAGAGATCACTGGCTGAAGGGTGGCATTATCGCGCGCGAC 720
Db 661 CTGACGGGAAGACCTACAGAGATCACTGGCTGAAGGGTGGCATTATCGCGCGCGAC 720
QY 721 AGCTGGTGACTGTGTGCGCCAACTAGCGGACCGGAGATCGCTCCGATGCGCGCGCGGT 780
Db 721 AGCTGGTGACTGTGTGCGCCAACTAGCGGACCGGAGATCGCTCCGATGCGCGCGCGGT 780
QY 781 GTGGAGCTGGACACCGCTCATCCGCGCAAGGGCAITGAGGGCATTTGTAACGCATGGAC 840
Db 781 GTGGAGCTGGACACCGCTCATCCGCGCAAGGGCAITGAGGGCATTTGTAACGCATGGAC 840
QY 841 ATTGAGGAGTGAACCCCAAGACCCGACAAAGTTCCTGTCTGCGCCCTACGACCAAGAACAGC 900
Db 841 ATTGAGGAGTGAACCCCAAGACCCGACAAAGTTCCTGTCTGCGCCCTACGACCAAGAACAGC 900
QY 901 GTCTAGCGCGGCAAGGCCGCCGCGGCAAGGAGGCGCTTCGAGGCGGAGTGGGCTGCTGTG 960
Db 901 GTCTAGCGCGGCAAGGCCGCCGCGGCAAGGAGGCGCTTCGAGGCGGAGTGGGCTGCTGTG 960
QY 961 GACCCCAACCGCCCGCTGTTCGCTTCATCGCGCGCTTCGAGGAGCAGAGGCTGTGGAC 1020
Db 961 GACCCCAACCGCCCGCTGTTCGCTTCATCGCGCGCTTCGAGGAGCAGAGGCTGTGGAC 1020
QY 1021 ATCATCTGGCGCCCTGCCCCAAGATCTTGGCCACCCCAAGGTGCAGATCGCCATCTCTG 1080
Db 1021 ATCATCTGGCGCCCTGCCCCAAGATCTTGGCCACCCCAAGGTGCAGATCGCCATCTCTG 1080
QY 1081 GGTACCGGCAAGGCCGCTTACGAGAAGCTGGTGAACGCCATCGGACCAAGTACAAGGCG 1140
Db 1081 GGTACCGGCAAGGCCGCTTACGAGAAGCTGGTGAACGCCATCGGACCAAGTACAAGGCG 1140
QY 1141 CCGCGCAAGGGCTGTGTAAGTTCCTCGCGCCCTTCGCGCACATGCTCACCGCGCGCGC 1200
Db 1141 CCGCGCAAGGGCTGTGTAAGTTCCTCGCGCCCTTCGCGCACATGCTCACCGCGCGCGC 1200
QY 1201 GACTTCATCTGTGGTCCCTTCGAGCCCTTCGAGCCCTGCGGCTGATCCAGCTGCACGCCATG 1260
Db 1201 GACTTCATCTGTGGTCCCTTCGAGCCCTTCGAGCCCTGCGGCTGATCCAGCTGCACGCCATG 1260
QY 1261 CACTACGGTACCGTCCCGCTGTAGCTCCACCGCGGCTGTGTCACACCGTCAAGGAG 1320
Db 1261 CACTACGGTACCGTCCCGCTGTAGCTCCACCGCGGCTGTGTCACACCGTCAAGGAG 1320
QY 1321 GCGCTCACCGGCTTCCACATGGCGCCCTGAACCCCGACAAAGCTGACGAGGTGACGCC 1380
Db 1321 GCGCTCACCGGCTTCCACATGGCGCCCTGAACCCCGACAAAGCTGACGAGGTGACGCC 1380
QY 1381 GACGCCCTGGCCCGACCGCTGCGCGCTGCCAGGAGGTGTTTCGCGGCGCGCGCTACCCC 1440
Db 1381 GACGCCCTGGCCCGACCGCTGCGCGCTGCCAGGAGGTGTTTCGCGGCGCGCGCTACCCC 1440
QY 1441 GAGATGGTGGCCAACTGCATAGCGAGGACCTGTCTGTGTCCAAAGCCCGCCAGAGTGG 1500
Db 1441 GAGATGGTGGCCAACTGCATAGCGAGGACCTGTCTGTGTCCAAAGCCCGCCAGAGTGG 1500
QY 1501 GAGGGCTCTGCTGGAGGAGGTGGTGTACGGCAAGGGCGGCTGGCCACCCCGCCAGAGGAG 1560
Db 1501 GAGGGCTCTGCTGGAGGAGGTGGTGTACGGCAAGGGCGGCTGGCCACCCCGCCAGAGGAG 1560

```
QY 1561 GAGATCAAGGTCGCCGTTGGTCCGAGAGATCCCC 1593
|||||
Db 1561 GAGATCAAGGTCGCCGTTGGTCCGAGAGATCCCC 1593

RESULT 6
LOCUS AX049327 1314 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 6 from Patent WO071734.
ACCESSION AX049327
VERSION AX049327.1 GI:12226094
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Location/Qualifiers
1..1314
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="fragment de l'DNAC complet codant la GBSSI de
Chlamydomonas reinhardtii"
<1..>1314
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC21782.1"
/db_xref="GI:12226095"
/translation="ALDIVMAAEVAPMSKGGDVTGGGLPIELVKRHRVMTIAPR
YDQYADAWDTSVVDIMGEKRYFHSIKGYHVRWIDHPWELAKWGTGSKLYGPRS
GADYDNRKALFKCAALEARVLPFGEDCFVANDWHSALVFLIKDEIQRGQ
FTKAKSLAINIAPQGRMWEAFKDLPOAFDFKLAIFSADYAKVYIATEPMEDEK
PPLTKYTKIINWKGIIADKLVTSPNATETADAGGVDELDTVIRAKIGIIV
NGMDLEENKPTDFLSAPYQNSVYAKAAKEALQALGLPVDPTAPLFAFIRLE
EOKGVDDIILAALPKIAPKQVQIALIGTGAAYEKLVNAIGTKYGRAGVYKFSAPL
AHMLTAGDFMIVSRFEPCGLIOLHAMHYTVPVVASTGGLVDIV"
BASE COUNT 238 a 449 c 408 g 219 t
ORIGIN
Query Match 67.3%; Score 1314; DB 6; Length 1314;
Best Local Similarity 100.0%; Pred. No. 1.7e-121;
Matches 1314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTGGACATCGTATGTTGCTGCTGAGTGCGCCCTTGTCCCAAGACGGCGCCCTG 60
|||||
Db 1 GCCTGGACATCGTATGTTGCTGCTGAGTGCGCCCTTGTCCCAAGACGGCGCCCTG 60
|||||
QY 61 GCGATGTGACTTGGTGGCTGCTATTGAGTGGTCAAGCGGGCCACCGCGTCATGACC 120
|||||
Db 61 GCGATGTGACTTGGTGGCTGCTATTGAGTGGTCAAGCGGGCCACCGCGTCATGACC 120
|||||
QY 121 ATTGCCCTCGCTACGACCAAGTACGCTGACGCTGGGACACCTCGGTGGTGGGACATC 180
|||||
Db 121 ATTGCCCTCGCTACGACCAAGTACGCTGACGCTGGGACACCTCGGTGGTGGGACATC 180
|||||
QY 181 ATGGGGGAGAAGTCCGCTTACCTCCACTCCATCAAGAAGGGGTGCAACCGGTGTGATT 240
|||||
Db 181 ATGGGGGAGAAGTCCGCTTACCTCCACTCCATCAAGAAGGGGTGCAACCGGTGTGATT 240
|||||
QY 241 GACCAACCCCTGTTCTTGCCCAAGTCTGGGGCAAGACCGGCTCCCAAGCTGTACGGCCCG 300
|||||
Db 241 GACCAACCCCTGTTCTTGCCCAAGTCTGGGGCAAGACCGGCTCCCAAGCTGTACGGCCCG 300
|||||
QY 301 CGCTCGGGCGCTGACTACCTGGACACACACAGCGGCTTCCGCTGTTCGCAAGGCCGCT 360
|||||
Db 301 CGCTCGGGCGCTGACTACCTGGACACACACAGCGGCTTCCGCTGTTCGCAAGGCCGCT 360
|||||
QY 361 ATTGAGGCTCGCGCGCTGCTGCTCGCCCTTCGCGCGGGGAGGACTGCGCTCTTCGTGGCCAAC 420
|||||
```

```
Db 361 ATTGAGGCTCGCGCGCTGCTGCTCGCCCTTCGGCCCGGGGAGGACTGCGCTTCGTGGCCAAC 420
|||||
QY 421 GACTGCACTCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
|||||
Db 421 GACTGCACTCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
|||||
QY 481 TTACCAAGGCGCAAGTGGTGGTATCCCAACATGCCCTTCAGGGCCGCGCATGTGG 540
|||||
Db 481 TTACCAAGGCGCAAGTGGTGGTATCCCAACATGCCCTTCAGGGCCGCGCATGTGG 540
|||||
QY 541 GAGGAGGCTTTCAAGACAGAGTGGCCCGCCAGGCGCTTTTGACAAGTGGCTTCTCG 600
|||||
Db 541 GAGGAGGCTTTCAAGACAGAGTGGCCCGCCAGGCGCTTTTGACAAGTGGCTTCTCG 600
|||||
QY 601 GAGGCTATGCCAAGTGTACACTGAGGCGCACCCCGCATGAGGACGAGAGACGAGAGCCCGG 660
|||||
Db 601 GAGGCTATGCCAAGTGTACACTGAGGCGCACCCCGCATGAGGACGAGAGACGAGAGCCCGG 660
|||||
QY 661 CTGACGGGAAAGACCTACAAGAGATCAACTGGCTGAAGGGTGGCATTTATCGCCGCGAC 720
|||||
Db 661 CTGACGGGAAAGACCTACAAGAGATCAACTGGCTGAAGGGTGGCATTTATCGCCGCGAC 720
|||||
QY 721 AAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
|||||
Db 721 AAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
|||||
QY 781 GTGGAGCTGGACACCGCTCATCCGCGCAAGGGCATTTGAGGGCATTTGTAACGCGCATGGAC 840
|||||
Db 781 GTGGAGCTGGACACCGCTCATCCGCGCAAGGGCATTTGAGGGCATTTGTAACGCGCATGGAC 840
|||||
QY 841 ATTGAGGAGTGGAAACCCCAAGACCGCAAGTTCCTGCTGCTGCGCCCTACGACCAAGACAGC 900
|||||
Db 841 ATTGAGGAGTGGAAACCCCAAGACCGCAAGTTCCTGCTGCTGCGCCCTACGACCAAGACAGC 900
|||||
QY 901 GTCTACGCGCGCAAGCGCCCGCCCAAGAGGGCCCTTCAGGCCCGAGCTGGSCCTTGCCTGTG 960
|||||
Db 901 GTCTACGCGCGCAAGCGCCCGCCCAAGAGGGCCCTTCAGGCCCGAGCTGGSCCTTGCCTGTG 960
|||||
QY 961 GACCCACACCGCCCGCTGTTGCGCTTTCATCGCGCGCTGAGGAGGAGAGGGTGTGGAC 1020
|||||
Db 961 GACCCACACCGCCCGCTGTTGCGCTTTCATCGCGCGCTGAGGAGGAGAGGGTGTGGAC 1020
|||||
QY 1021 ATCATCTGCGCCCGCTGCGCCCAAGATCTTGGCCACCCCGCAAGGTGAGATCGCCATCCTG 1080
|||||
Db 1021 ATCATCTGCGCCCGCTGCGCCCAAGATCTTGGCCACCCCGCAAGGTGAGATCGCCATCCTG 1080
|||||
QY 1081 GGTACCGCAAGCGCCCGCTACGAGAGTGGTGAAGCCCATCGCCACATGCTCACCGCGCGCC 1140
|||||
Db 1081 GGTACCGCAAGCGCCCGCTACGAGAGTGGTGAAGCCCATCGCCACATGCTCACCGCGCGCC 1140
|||||
QY 1141 CGCGCCCAAGGGCGTGGTCAAGTTCCTGCGCGCCCTGCGCGCACATGCTCACCGCGCGCC 1200
|||||
Db 1141 CGCGCCCAAGGGCGTGGTCAAGTTCCTGCGCGCCCTGCGCGCACATGCTCACCGCGCGCC 1200
|||||
QY 1201 GACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
|||||
Db 1201 GACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
|||||
QY 1261 CACTACGCTACCGTGGCGCTGAGGCTTCCACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1314
|||||
Db 1261 CACTACGCTACCGTGGCGCTGAGGCTTCCACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1314
|||||
```

```
RESULT 7
LOCUS AF433156 5856 bp DNA linear PLN 23-AUG-2002
DEFINITION Chlamydomonas reinhardtii granule-bound starch synthase I (STA2)
ACCESSION AF433156
VERSION AF433156.1 GI:16755882
KEYWORDS Chlamydomonas reinhardtii.
```



```
QY 929 AGGCCTCGAGCCGAGCTGGGCTGCTGTGGAACCCACCACCCGCTGTTCGCTTCA 988
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1136 AGGCCTCGAGCCGAGCTGGGCTGCGGTGGACAGGAGTGGCTGTTCGCTTCA 1195
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 989 TCGGCGGCTCGAGGAGCAGAGGCTGTGGACATCATCTGCGCGCCCTGCGCAAGATCC 1048
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1196 TCGGCGGCTCGAGGAGCAGAGGCTGTGGACATCATCTGCGCGCCCTGCGCAAGATCC 1255
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1049 TGGCCACCCCAAGCTGCAGATCGCATCTCTGGGTACCGGCAAGCGCGCTACGAGAAGC 1108
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1256 TGAAGGAGGAGACCTCCAGATCATCTCTTGGACCGGGAAGAGTGTGAGAAGC 1315
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1109 TGGTGAACCCCATCGCACCAAGGCGCGGCCCAAGGCGCTGTGCAAGTTCGCG 1168
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1316 TGTCTAAGAGCATGAGGAGAGTTCGCGGCAAGTGTGAGGCGGTGAGTTCACAG 1375
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1169 CGCCCTCGGCGACATGCTCACCGCGCGCGGCTTCACTGCTGCTGCGCTGCGCTTCG 1228
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1376 CGCCGCTAGCTCACCAGATGATGCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1435
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1229 AGCCCTGCGGCTGATCCAGCTGCAGCGCATGCTACGCTACGCTGCGGCTGCTGCTG 1288
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1436 AGCCCTGCGGCTGATCCAGCTGCAGCGCATGCTACGCTACGCTGCGGCTGCTGCTG 1495
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1289 CCACCGCGGCGCTGCTGCGACACCGTCAAGGAGGCGCTCACCGGCTTCCACATGGGCGGCC 1348
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1496 CCACCGCGGCGCTGCTGCGACACCGTCAAGGAGGCGCTCACCGGCTTCCACATGGGCGGCC 1555
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1349 TGA-----ACCCGACAGCTGAGGAGTGCAGCGCATGCTACGCTACGCTGCGGCTGCTGCTG 1402
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1556 TCAGCGTCACTGCAACGCTGCTGCGGCGCGGCTGAGAGGCTGAGAGGCTGCGGACCACTGA 1615
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1403 GCGTGCAGGAGGCTGCTGCGGCGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTG 1462
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1616 AGCGGCGCTGAGGCTGCTGCGGCGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTG 1675
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1463 GCAGGACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1522
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1676 TCAGGATCTCTCTGAGAGGAGCTGCTGAGAGGAGCTGCTGAGAGGAGCTGCTGAGAGGAGCTG 1735
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1523 TGACGCGAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1736 GGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1773
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 10
HWAXYR
LOCUS HWAXYR 2311 bp mRNA linear PLN 12-SEP-1993
DEFINITION Barley mRNA pcwx27 for waxy locus.
ACCESSION X07932
VERSION X07932.1 GI:19128
KEYWORDS starch synthase; waxy locus.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 2311)
Zohde,W
Direct Submission
Submitted (21-JUN-1988) Zohde W., Max Planck Institute, Erwin Baur
Institut, D-5000 Koln 30, FRG
REFERENCE 2 (bases 1 to 2311)
Rohde,W., Becker,D. and Salamini,F.
Structural analysis of the waxy locus from Hordeum vulgare
Nucleic Acids Res. 16 (14B), 7185-7186 (1988)
88303345
2970062
PUBMED
COMMENT The sequence overlaps with the genomic sequence of the waxy locus,
x07931, from bp 1918 to bp 2301.
FEATURES
source 1..2311
```

```
/organism="Hordeum vulgare subsp. vulgare"
/strain="Vogelsanger Gold"
/db_xref="taxon:112509"
/map="chromosome 1"
/clone="pcwx27"
/clone_lib="EMBL4"
CDS
226..2037
note="starch synthase"
/codon_start=1
/protein_id="CAA30756.1"
/db_xref="GI:19129"
/db_xref="SWISS-PROT:P09842"
/translation="MAALATSLATSGTVLGYDRFRPFGFGLRPNPADALGMRT
IGASAPKQSRKRAHGRSRCLSVVVSATSGSMNLVFGAEMAPWKTGGLGSLP
PAMAANGHRVWVVSPPYDOYKADMTSVISEIKVADEVERFHCYKRGVDRVIDH
PWFLEKVRGKTKETIYGPADGTDYDNOQFSLCQAALAPRIILNKNRYFSGPYG
EDVWPCNDWHTKTLACYLKNYQNGIYRTAKVAFCHNIYQGRFSPDDFAQLNLP
DRFKSDFIDGYDKPVEGRKINMKAGILOADKVLTVSPYAEELISGEARGCELDN
IMRLGITGVNGMDVSWDPDKFELAVNYDITVTALEKALNKEKLAKALEVGLPVDK
VPLVAFIGRLERQKGPDMIAIPILKEEDVQIILLCTGKKFKLLKMSKEKPGK
VRVVRFNAPLAHQMHAGADLLAVSRFEPCGLIQLOGRYGTGTCVCASTGSGIVTIV
EGKTFHMRGLSVDENVVADVKVATTLKRAVKVGPAYQEMVKNCMIQDLSWK
PAKNVEDVLLELGVSESGPIVGEHIAPIAMENVAAP"
2276
note="poly A site (pcwx4)"
2283
note="poly A site (pcwx27)"
2301
note="poly A site (pcwx18)"
BASE COUNT 501 a 688 c 714 g 403 t
ORIGIN
Query Match 27.1%; Score 530; DB 8; Length 2311;
Best Local Similarity 61.6%; Pred. No. 4,7e-44;
Matches 985; Conservative 0; Mismatches 520; Indels 93; Gaps 5;
QY 5 TGCACATCGTGATGTTGCTGTGAGTCCGCTTGGTCCCAAGACGGCGGCTGGCG 64
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 452 TGRACCTCGTGTGTCGCGCGCGAGATGGCGCTCGAGCAAGACCGCGGCTTGCG 511
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 65 ATGTGACTGTGGCTGCCTTATTGAGTGTGTCAGCGCGGCGACCGGCTGATGACCATG 124
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 512 ATGTCTCTCGCGGCTCCCGCGCCATGGCGGCAACGGTCAACGGGTGATGTCGTCT 571
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 125 CCCTCTCGTAGCAGTACGCTGAGCGCTGGGACACTCGGTGCTGTGACATCATGG 184
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 572 CCGCGCTACGATCAGTCAAGACGCGCTGGGACACGCGGTATCTCCGAGATCAAG 631
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 185 -----GGGAGAAGTTCGCTTCTCCACTCCATCAAGAAGGCGCTGACCGCG 232
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 632 TCGCTGACGAGTACGAGGAGGTGAGTTCCTCCACTGCTACAGCGGAGTGGACCGCG 691
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 233 TGTGATTTGACACCCCTGCTGCTGCGCAAGTCTGGGGCAAGACCGGCTTCAAGTGT 292
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 692 TGTTCATCGACACCCCTGCTGCTGAGAGAGTCCGGGGCAAGACCAAGAGAAGATCT 751
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 293 ACGGCCCCGCTCGGCGCTGCTACCTGGGACACCAAGCGCTGCGCGCTGCTGCA 352
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 752 ACGGCCCCGCTCGGCGCTGCTGCTGAGAGAGTCCGGGGCAAGACCAAGAGAAGATCT 811
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 353 AGGCGCTTATTGAGGCTGCGCGCTGCTGCGCTTC-----G 388
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 812 AGGCGACTGAGGCGACCCAGGATCTCAACCTCAACAACCCCTTCTTCTGCTC 871
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 389 GCGCGCGGAGGACTGGTCTTGTGGCCAAAGCTGCGACTCGCGCTGCGCGCTGCG 448
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 872 CTTACGGGGAAGACGTGGTGTGCTGCTGCAACGACTGGCACACGCGGCTTCTGGCTCT 931
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 449 TGTGAGGAGGACTTACAGCCAGGCGGCTTCAACCAAGGCGGAGTGTGCTGCTCA 508
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 932 ACCTCAAGAGCAACTACAGTCCCAATGGCATCTACAGGACGCGGAGGTGGCTTCTGCA 991
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 509 TCCACACATCGCTTCCAGGCGCGCTGCTGGGAGGAGGCTTCAAGGACACAGAGCTGC 568
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```



```

|||||
992 TCACAACTCTCGTACAGGCGCGTTCCTTCGAGACTTTGGCAGCTCAACTGC 1051
QY CCAGAGCGCGCTTTGACAACTGGCTTCGAGAGCGCTATGCCAAGTTTACACTGAGG 628
Db CCAGAGGTTCAAGTCGTCTTCGACTTATTCAGCGCTACGACAAG----- 1098
QY CCACCCCATGAGGAGGACGAGAACGCCCGCGCTGACGGGAAGACCTACAGAAGATCA 688
Db -----CCCGTGGAGGGCG-----AAGATCA 1120
QY ACTGGCTGAAGGTGGCAATTATCCGCGCGACAAAGCTGTGACTGTGTCGCCCACTAAG 748
Db ACTGGATGAAGCGCGGATCCTCAGGCGCGACAAAGTGTGACGGTGAGCCCTACTACG 1180
QY CGACCCAGATCGCTCGCGATCCCGCGCGGTGTGAGCTGGACACGCTCATCCGCGCCA 808
Db CTGAGAGGCTCATCTCTGGCGAAGCCGAGGGGTGCGAGCTCGACAACATCATCGGCTCA 1240
QY AGGCAATTGAGGCGATTGTGAAGCGCATGCACATTGAGGAGTGGAAACCCCAAGCGACA 868
Db CGGGATCACCGGAATCGTCAAGCGCATGACCTCAGTGAAGTGGGACCCCAAGGACA 1300
QY AGTTCCTGTCTGCGCTACGACCAAGACAGCGCTCTACGCGCGCAAGCGCGCCAAAGG 928
Db AGTTCCTGCGCTCAACTACGACATCACACCGCGTTTGGAGCCAGGCGCTGAACAAG 1360
QY AGGCGCTGACGCGCGAGCTGGGCTGCTGTGACATCATCTGCGCGCGCTGCCCAATCC 1048
Db TCGGAGGCTGAGGAGCAGAGGCGCGCGAGTGAATCGCGCGCATCCCGGAGATCC 1480
QY TGGCACCCCGCAAGTGTGAGATCGCCATCTCTGGGTACCGGCAAGCGCGCTACGAGAAG 1108
Db TGAAGGAGGAGGACGCTCCAGATCATCTCTTGGCACCGGGAAGAAGATTGAGAAG 1540
QY TGGTGAACGCCATCGCCACCAAGTACAAAGGCGCGCGCCAAAGGGGTGTGATGCTCGG 1168
Db TGCTCAAGAGCATGAGGAGGAAGATTCCCGGGAAGGTGAGGCGCGCTGTGAGTTCAAG 1600
QY GCGCGCTGCGCACATGCTCAAGCGCGCGCGCTTCAATGCTGCGCTGCGCGCTGCGG 1228
Db GCGCGCTAGCTCACCATGATGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1660
QY AGCCCTGCGGCTGATCCAGCTGACGCGATCGCATGAGGTACCGTACCGTGGGTAGCGT 1288
Db AGCCCTGCGGCTGATCCAGCTGACGCGATCGCATGAGGTACCGTGGGTAGCGT 1720
QY CCACGCGCGCTGCTGACACCGCTCAAGGAGGCGCTCACCGGCTTCCACATGGGCGCC 1348
Db CCACGCGGCGCTGCTGACACCGCTGAGGAGGCGCTCAAGGAGGCGCTTCCACATGGG 1780
QY TGA-----ACCCGACAAAGTGGACGAGGCTGACGCGCGAGCCCTGCGCGCACCGTGC 1402
Db TCAGCGTCCGACTGCAACGCTGTGAGCGCGCGAGCTGAAGAGTGTGGGACCCCTGA 1840
QY GCGTGCAGGAGGTGTTTGGGCGCGCGCTACCCGAGATGTTGGCCCACTCATCA 1462
Db AGCGGCGCGTCAAGTGTGCGCGCGCGCGCTTACAGGATGTTCAAGAACTCATCA 1900
QY GCGAGGACTGCTCTGTTGTTGCGCGCGCGCTACCCGAGATGTTGGCCCACTCATCA 1522
Db TCCAGGATCTCTCTGGAAGGACCTGCAAGAACTGGGAGGAGTGTGTTGGAACCTG 1960
QY TGTAGCGAAGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1560
Db GGTGGAGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1998

```

RESULT 11

```

AF486515 1827 bp mRNA linear PLN 02-JUL-2002
LOCUS Hordeum vulgare cultivar waxy oderbrucker granule bound starch
DEFINITION synthase I mRNA, complete cds.
ACCESSION AF486515
VERSION AF486515.1 GI:21667429
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 1827)
AUTHORS Patron, N., Smith, A., Fahy, B., Hylton, C., Naldrett, M., Rossnagel, B.
and Denyer, K.
TITLE A mutation in the 5' non-coding region of the barley GBSI gene
alters its temporal and spatial expression and reduces GBSI
activity and amylose content in the endosperm
UNPUBLISHED
2 (bases 1 to 1827)
PATRON, N.
DIRECT SUBMISSION
SUBMITTED (22-FEB-2002) Metabolic Biology, John Innes Centre,
Norwich Science Park, Norwich, Norfolk NR4 7UH, UK
LOCATION/QUALIFIERS
1. 1827
/organism="Hordeum vulgare"
/cultivar="waxy oderbrucker"
/db_xref="taxon:4513"
1. 1827
/note="alpha glycosyl transferase"
/codon_start=1
/product="granule bound starch synthase I"
/protein_id="AA074049.1"
/db_xref="GI:21667430"
/translation="MAALATLSQATSGTVLGVTDTSAPSMFRHAGFQGLRPRKPADGT
FMRTVGSAAAPKQSKAHNRNRLSVVRATGSMNLVFGAAMAPWSKVTGGLGDV
LGGLPMAAANGHRVYVSPRYDQKADMTSVISEIKVADEYKVRPHCYKRGVDR
VFIDHFWLEKVRGKTKETIGPDAGTDEDNQRFSLCCOALEPRLINNNPYF
SPYGEDVVCNDMHTGLIACLYKSNOSNGIYAKVAFCHINISYQGRSFDDFA
QLNLPDRKSSDFDIDGDKPVEGRKINMKAGILQADKLVFVSPYAEELISGEARG
CELDNMLRIGITGVNGDVSEMDPTKDKFLAVNYDITALEAKALKEALQAEVGL
PVDKRPILVAFIGLEQEGKDPVMTAAIPEILKEEDVQILIGTKKFKLLKSMEE
KFGKRVAVRFNAPLAHOMAGADLLAVTSFEPGLIQLQGMRYGTPCVCASTGGL
VDTIVGKTFHMRSLVDCNVPADVKVATITLRAVKVVGTPAYQDMYKNCMIQD
LSWKGPAKNWEDVLELGVGSEPGIVGEIETAPLAVENVAAP"
BASE COUNT 364 a 567 c 602 g 294 t
ORIGIN
Query Match 27.1%; Score 528.4; DB 8; Length 1827;
Best Local Similarity 61.6%; Pred. No. 7.2e-44;
Matches 984; Conservative 0; Mismatches 521; Indels 93; Gaps 5;
QY 5 TGGACATCGTGTGTTGCTGCTGAGTGCCTTGGTCCAGAGCGGCGCTGGCG 64
Db 242 TGAACCTCGTGTTCGTCGCGCGCGAGATGGCGCTTGGAGCAAGACCGCGCTGGCG 301
QY 65 ATGTGACTGTGCTGCTTATTGAGTGTGCAAGCGCGCCACCGCTCATGACCATTTG 124
Db 302 AGCTCTCGCGCGCTTCCACAGCATGGCGCCACCGTACCGGGTGTGGTCTGCT 361
QY 125 CCCCTCGCTACGACAGTACGCTGACGCTGGGACACCTCGGTGCGTGGACATCATGG 184
Db 362 CCCCGCGCTACGATCAGTACAGGACGCGCTGGACACCGAGCTCATCTCCGAGATCAAG 421
QY 185 -----GCCAGAGGTCCGCTACTTCCACTCCATCAAGAAAGCGCGTGCACCGG 232
Db 422 TCGCTGACGAGTACGAGAGGAGGTGAGTCTTCCACTGTACAAAGCGCGAGTGGACCGG 481
QY 233 TGTGATGACCAACCCCTGTTCTCTGGCCCAAGTCTGCGGCAAGACCGGCTCCCAAGCTGT 292
Db 482 TGTTCATCGACCAACCCCTGTTCTCTGGAGAGGTCCGCGGCAAGAGAGATCT 541

```

Db	1571	TCAGCGTGCAGCTGAGAGTGGAGCCGCGGACGTGAAGAAGTGGCGCACCACTGTA	1630
QY	1403	GCCTGCCACGAGTGTGTCGGGGCGCGCTACCCCGAGATGGTGCACCACTGCATCA	1462
Db	1631	AGCGGCGGTCAAGGTGCTGCGGACGCGCGCGTACAGGAGATGGTCAAGAAGTGCATGA	1690
QY	1463	GCAGAGACCTGTCTGTGTCGAAGCCGCCCCAGAGTGGAGGGGCTCTCTGGAGAGTGG	1522
Db	1691	TCCAGATCTCTCTGGAAGGACCTGCCAAGAACTGGGAGGAGTCTTCTGGAAGTGG	1750
QY	1523	TGTACGCAAGGGCGCGTGGCCACCGCCCAAGAAGGAG	1560
Db	1751	GGGTGGAGGAGCGGAGCGCGGATGCTCGCGGAGGAG	1788
RESULT 12			
LOCUS	AF486518	1827 bp	mrna linear PLN 02-JUL-2002
DEFINITION	Hordeum vulgare cultivar SB 85750 granule bound starch synthase 1 mRNA, complete cds.		
ACCESSION	AF486518	1	GI:21667435
VERSION	Hordeum vulgare.		
KEYWORDS	Hordeum vulgare		
SOURCE	Hordeum vulgare		
ORGANISM	Hordeum vulgare		
REFERENCE	1 (bases 1 to 1827)		
AUTHORS	Patron, N., Smith, A., Fahy, B., Hylton, C., Naldrett, M., Rossnagel, B. and Denyer, K.		
TITLE	A mutation in the 5' non-coding region of the barley GBSSI gene alters its temporal and spatial expression and reduces GBSSI activity and amylose content in the endosperm		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 1827)		
TITLE	Direct Submission		
JOURNAL	Submitted (22-FEB-2002) Metabolic Biology, John Innes Centre, Norwich Science Park, Norwich, Norfolk NR4 7UH, UK		
FEATURES	Location/Qualifiers		
source	1..1827		
CDS	/organism="Hordeum vulgare"		
	/cultivar="SB 85750"		
	/db_xref="taxon:4513"		
	1..1827		
	/note="alpha glycosyl transferase"		
BASE COUNT	364 a 567 c 602 g 294 t		
	ORIGIN		
Query Match	27.1%; Score 528.4; DB 8; Length 1827;		
	Best Local Similarity 61.6%; Pred. No. 7.2e-44;		
	Matches 984; Conservative 0; Mismatches 521; Indels 93; Gaps 5		
QY	5	TGGACATCGTATGCTGCTGAGTGCGCCCTTGGTCCCAAGACGGCGGCGCTGGCGG	64
Db	242	TGAACCTCGTGTCTGTCGGCCGAGATGGCCCTTGGAGCAGACCGCGGCTTGGCG	301

/protein_id="AAF34135.1"
/db_xref="GI:696978"
translation="MAALVTSQATSGVLTGTTDFRRAGFGVRRPRPADAAALGMRT
VGASAAPTQSKAHKTRCLSMVVRATSGSMNLVFCVGAEMAPWSKTKGLDVLGGL
PPMAANGHRVTKISPRDQKADMTDSVSEIKVVDYKRYRPHCHNLDNNDFYVD
HPCFLKVRGTRKELIGPDAGTDYEDNQRFSLCCQAALVPRFHLNLDNNDFYVD
GDDVYFVNDHMTGLLALYKLSNSNGIYRAAKVAFCHNI SYGRFSFDDPAQLNL
PDRFKSSPFDIGDKPVGRKINNMKAGILQADKLVSPYAYBELISGEARGCELD
NIMRLTGITGVNGMDVSEMDPTKDFELAVNDITTALEKALNEALQAEVGLPVDL
KVPVAFIIGRLKEQKPDVMTAAIPEILKEEDVOIIVLLGCTKKFERLLKSTFEKPPS
KYRVAFRNAPLHOMAGADVLAIVSRFEPGGLIOLQGMRYGTPCASCASUGGLVDIT
VEGKTFHMFHRLSDVNCVNEPADVKKVITLKRKVVVGTTPAYHEMVNKMOTDLSWK
GPKNNMDVLELGVGSEPGVIGIEIAPLAMENVAAP"
BASE COUNT 452 a 617 c 687 g 371 t
ORIGIN

Query Match 26.9%; Score 525.6; DB 8; Length 2127;
Best Local Similarity 61.4%; Pred. No. 1.3e-43;
Matches 1002; Conservative 0; Mismatches 534; Indels 96; Gaps 6;
QY 5 TGGACATCGTGTGCTGTGAGTCCGCCCTTGGTCCAAAGACGGCGGCTGGGG 64
DB 259 TGAACCTGTGTCTGCGCGCGCGAGATGGCGCTTGGAGCAAGACGGCGGCTGGCG 318
QY 65 ATGTGACTGTGGCCCTGCTATTGAGTGTGTCAAGCGCGGCCACCGGCTCATGACCATG 124
DB 319 ACCTGCTGGGGCTCCGCCAGCCATGGCGCCCAAGCCACCGGCTCATGTCATCT 378
QY 125 CCCCTCGCTACGACAGTACGTGACGCTGGGACACCTCGTGTGCTGGGACATATG 184
DB 379 CCCCGGCTACGACAGTACGAGGACGCTGGGACACACGCTGCTCCGAGATCAAG 438
QY 185 -----CGGAGAAGTCCGCTACTTCCACATCCATCAAGAAAGGGCGTCCACGG 232
DB 439 TCGTTGACAGTACGAGAGGTGAGGTACTTCCACTGCTACAGCGGGGTGGACGG 498
QY 233 TGTGAGTACACCCCTGCTTCTGGCCAAAGTCTGGGGCAAGACCGGCTCCAAAGTGT 292
DB 499 TGTGCTGACACCCGCTTCTGGAGAAGTCCGGGGCAAGACCAAGGAGAATCT 558
QY 293 ACGGCCCCGCTCCGGCGTACTACTGGACACACACAGCGCTCGCCCTGCTGCA 352
DB 559 ACGGGCGCGACCGCGCGAGGATAGAGGACCAACAGCAGCGCTTCAGCTTCTG 618
QY 353 AGCCGCTATTGAGGTGCGCGCGTGTGCTGCTG----- 388
DB 619 AGCGGCGTGAAGTCCGAGGATCCTGAACCTCGACATAACCCCTACTTTCTGGG 678
QY 389 GCGCGCGGAGGACTGGCTTCTGGCCCAAGCTGGGCACTCGCCCTGGTGGCGCTC 448
DB 679 CCTACGGGAGGAGTGGTGTCTGCAATGATGCTGACACACGGGCTTCTGGCGCT 738
QY 449 TGCTGAAGGACGAGTACACGCCCAAGGCGCAGTTTCAACAGGCGCAAGTGTGCTGCTA 508
DB 739 ACCTCAGACCACTACCATGCAATGGCATCTACAGGCGCGCAAGGTGCATCTGCA 798
QY 509 TCCACAACTGCGCTTCCAGGCGCATGTGGAGGAGGCTTTTCAAGACACGAAGTGC 568
DB 799 TCCACAACTGCTGACAGGCGGCTTCTGCTGCAATGATGCTGACACACGGGCTTCTG 858
QY 569 CCAGGCGCGCTTGTGACACTGCGCTTCTCGGACGCTATGCCAAGGTTTACACTGAG 628
DB 859 CCAGACAGTTCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 905
QY 629 CCACCCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 688
DB 906 -----CCGGTGGAGGCGC----- 927
QY 689 ACTGGCTGAAGGTTGGCATTTATCGCCCGCGACAGCTGCTGCTGCTGCTGCTGCTG 748
DB 928 ACTGATGAAGGCGCGGATCTGTCAGGCGCGACAGAGTGTGCTGCTGCTGCTGCTG 987
QY 749 CGACCGAGATCGTGTCCGATCCCGCGGCTGTGTGGAGTGGACACCGCTCATCGCGCA 808

DB 988 CGGAGAGCTCATCTCTGGCGAAGCAGGGGCTGCGAGCTCGACACATCATCGGCTCA 1047
QY 809 AGGGCAITGAGGCGCATTTGTGAACGGCATGACATTTAGGAGTGAACCCCAAGACCGACA 868
DB 1048 CTGGGATCACCAGCATCTGCAACGGCATGATGTAGCGAGTGGACCCCAAGGACA 1107
QY 869 AGTTCTGTCTGCGCCCTAGCACCAAGAACAGCGCTTACGCCGGCAAGCGCGCGCAAG 928
DB 1108 AGTTCTGCGCGTCAACTACGACATCACCACCGCTTGGAGGGAAGAGCGCTGAACAAG 1167
QY 929 AGCCCTGAGGCGAGCTGGCGCTGCTGTGACCCCAAGCGCGCGCGCTGCTGCGCTTCA 988
DB 1168 AGCGCTGACGCGGAGTGGCGCTGCGGTGCGCGAAGGTGCGCGCTGCTGCGCTTCA 1227
QY 989 TCGCGCGCTTGGAGGAGCAAGGCTGTGACATCATCTTGGCGCGCTTCCCAAGATCC 1048
DB 1228 TCGGAGGCTGGAGGAGCAAGGCGCGCGCTGATGATGCGCGCATCCGAGATCC 1287
QY 1049 TGCCCAACCCCAAGGTGACATCGCCATCTGCTGAGTACCGCAAGCGCGCTTACGAGAC 1108
DB 1288 TGAAGGAGGAGGACGCTCAGATCTTCTCTGGGCAACCGGAAGAGAGTTGCGAGCG 1347
QY 1109 TGTGACGCGCATCGGCACCAAGTACAAGGCGCGCGCGCGCTGCTCAAGTCTCTCG 1168
DB 1348 TACTCAAGAGCATTTGAGGAGAAATCCCGAGCAAGTGAAGGCGCTGCTGAGTCAACG 1407
QY 1169 CGCCCTTGGCGCATGCTCACCGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1228
DB 1408 CGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1467
QY 1229 AGCCCTGCGCGCTGATCCAGCTGCAACCGCATGCTGCTGCTGCTGCTGCTGCTGCTG 1288
DB 1468 AGCCCTGCGCGCTCATCCAGTCCAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTG 1527
QY 1289 CCACCGCGCGCTTGTGCTGACACCGCTCAAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTG 1348
DB 1528 CCACCGCGCGCTTGTGCTGACACGATCTGAGGCGCAAGCGCTTCCATGAGCGCGG 1587
QY 1349 TGA-----ACCCCGCAAGCTGACGAGGCTGACCGCGCTGCTGCTGCTGCTGCTGCTG 1402
DB 1588 TCAGTGTGATTCGACAGTGTGAGCGCGCGCGCTGAGAGAGTGTGACACCGCTGA 1647
QY 1403 GCGGTGCGAGGAGTGTGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1462
DB 1648 AGCGCGCGCTCAAGTGTGCTGCGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1707
QY 1463 GCCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1522
DB 1708 TACAGGATCTCTGCTGAGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1767
QY 1523 TGTACGCAAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1582
DB 1768 ---GTGTCGAGGCGGAGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1824
QY 1583 AGAAGATCCCG 1594
DB 1825 AGAAGTCCCG 1836

RESULT 14
AF486519
LOCUS
DEFINITION
AF486519
VERSION
KEYWORDS
SOURCE
ORGANISM
AF486519
Hordeum vulgare cultivar CDC Alamo granule bound starch synthase 1
mRNA, complete cds.
AF486519.1 GI:21667437
Hordeum vulgare.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.

Db 1691 TCCAGGATCTCTCTGGAAGGACCTGCCAAGAACTGGGAGGACGTGCTTCIGGAACTGG 1750

QY 1523 TGTAAGGCAAGGGCGGCGTGGCCACCGCCCAAGAGGAG 1560

Db 1751 GGTGGAGGAGCGAGCCGGGATCTGTCGGGAGGAG 1788

Search completed: June 3, 2003, 13:34:07
Job time : 3422.54 secs

This Page Blank (uspto)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 05:08:24 ; Search time 283.834 Seconds
(without alignments)
15495.523 Million cell updates/sec

Title: US-09-980-771A-4

Perfect score: 1953

Sequence: 1 gcctgacacatgctggt.....ccgccaccccaagtcgccc 1953

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002:*

1:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
17:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	704	36.0	1696	22 AAC86955
2	475.8	24.4	2267	18 AAC63355
3	471	24.1	1915	19 AAX60319
4	447.4	22.9	2542	19 AAV29753
5	316.8	16.2	2161	24 ABK53210
6	298	15.3	2115	21 ABK53215
7	256	13.2	2183	24 ABK53215
8	221	11.3	2807	21 AAC86435
9	221	11.3	2842	21 AAC86411

10	218.2	11.2	2826	19 AAV01528
11	216.8	11.1	2097	19 AAV29755
12	214.8	11.0	2423	19 AAV70958
13	214	11.0	2107	21 AAC86412
14	214	11.0	2107	21 AAC86434
15	212.4	10.9	9024	21 AAC86431
16	210.8	10.8	2380	19 AAV56834
17	210.2	10.8	2920	24 ABK88112
18	209.8	10.7	2478	18 AAT67287
19	209.2	10.7	2939	21 AAC86410
20	209.2	10.7	2939	21 AAC86433
21	208.6	10.7	2946	24 ABK88115
22	208.6	10.7	2951	24 ABK88114
23	208.2	10.7	2950	24 ABK88113
24	207	10.6	2248	21 AA250651
25	206.6	10.6	1798	21 AA250647
26	206.6	10.6	2019	21 AA250646
27	203.8	10.4	1724	24 ABA01821
28	161	8.2	2007	19 AAV70959
29	161	8.2	2007	19 AAT29754
30	161	8.2	2085	18 AAT67286
31	161	8.2	2085	19 AAV66833
32	151	7.7	1479	24 ABQ90258
33	151	7.7	1479	24 ABQ90406
34	125.6	6.4	333	21 AAC74569
35	125.6	6.4	333	24 ABN18316
36	118.2	6.1	2239	19 AAV01527
37	118.2	6.1	2805	21 AA224487
38	116	5.9	2662	20 AAX34651
39	110.8	5.7	65140	22 AAD17184
40	110.8	5.7	125401	22 AAD17186
41	110.6	5.7	2533	15 AAQ45183
42	108	5.5	1758	17 AAT32325
43	106.8	5.5	2277	19 AAV13836
44	106.8	5.5	2277	19 AAV05372
45	106.4	5.4	1984	21 AAC46597

ALIGNMENTS

RESULT 1

AAC86955

ID AAC86955 standard; cDNA; 1696 BP.

XX AAC86955;

XX AC

XX 02-APR-2001 (first entry)

DT cDNA encoding a granule bound starch synthetase II (GBSSII).

DE Granule bound starch synthetase II; GBSSII; starch grain;

XX adenosine diphosphate glucose-alpha1,4-glucan alpha4-glucosyltransferase;

KW starch synthetase; ds.

XX Chlamydomonas reinhardtii.

OS Key

XX Location/Qualifiers

FT CDS

FT /*tag= a

FT /product= "granule bound starch synthetase II (GBSSII)"

XX FR2793806-AL.

PN 24-NOV-2000.

XX 21-MAY-1999; 99FR-0006494.

XX 21-MAY-1999; 99FR-0006494.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Dhulst C, Ball S;

PI

```
XX DR WPI; 2001-052291/07.
XX DR P-PSDB; AAB31175.
XX PT New recombinant nucleic acid encoding fusion of starch synthase and
XX PT second component, useful in pharmaceutical and food compositions, is
XX PT targeted to starch granules -
XX PS Claim 3; Fig 1; 52pp; French.
XX CC The present sequence encodes a granule bound starch synthetase II
XX CC (GBSSI). The specification describes a recombinant nucleic acid,
XX CC comprising a polynucleotide encoding an adenosine diphosphate
XX CC glucose-alpha1,4-glucan alpha4-glucosyltransferase or starch
XX CC synthetase, placed upstream of a sequence that encodes a polypeptide
XX CC of interest. The adenosine diphosphate glucose-alpha1,4-glucan
XX CC alpha4-glucosyltransferase protein can migrate to sites of
XX CC biosynthesis of starch grains in plant cells, becoming associated
XX CC with these grains. The recombinant nucleic acid sequence is used to
XX CC target polypeptides of interest to starch grains.
XX SQ Sequence 1696 BP; 347 A; 509 C; 571 G; 269 T; 0 other;

Query Match 36.0%; Score 704; DB 22; Length 1696;
Best Local Similarity 100.0%; Pred. No. 7.6e-93;
Matches 704; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1250 TGCACGCCATGCACTAGCTACGTCGCGGTGTAGCTCCACCGCGGCTGGTGACA 1309
DB 13 TGCACGCCATGCACTAGCTACGTCGCGGTGTAGCTCCACCGCGGCTGGTGACA 72
QY 1310 CCCTCAAGGAGGCGTCAACGGCTTCCACATGGCGCCCTGACCCCGACAAGCTGACG 1369
DB 73 CCCTCAAGGAGGCGTCAACGGCTTCCACATGGCGCCCTGACCCCGACAAGCTGACG 132
QY 1370 AGCTGACGCCGACGCCCTGTGGCGCGCACCGTGTGCGCGTCCACGAGGTGTTTGGCGGG 1429
DB 133 AGCTGACGCCGACGCCCTGTGGCGCGCACCGTGTGCGCGTCCACGAGGTGTTTGGCGGG 192
QY 1430 GCCGCTACCCCGAGATGGTGGCCAACTGTCATCAGCAGGACCTGCTCTGTCTCAAGCCG 1489
DB 193 GCCGCTACCCCGAGATGGTGGCCAACTGTCATCAGCAGGACCTGCTCTGTCTCAAGCCG 252
QY 1490 CCAGAGTGGAGGCGCTCTGTGAGGAGTGTGTACGCAAGGGCGGCTGGCCACCG 1549
DB 253 CCAGAGTGGAGGCGCTCTGTGAGGAGTGTGTACGCAAGGGCGGCTGGCCACCG 312
QY 1550 CCAGAGGAGGAGATCAAGTCCCGTTCGCCAGAGATCCCGGGGACCTTGGCCGCG 1609
DB 313 CCAGAGGAGGAGATCAAGTCCCGTTCGCCAGAGATCCCGGGGACCTTGGCCGCG 372
QY 1610 TGTCTACGCCCCCAACACCCCTGAAGCCGCTGTCCGCTCCGTGTGAGGGCAAGCGCGCG 1669
DB 373 TGTCTACGCCCCCAACACCCCTGAAGCCGCTGTCCGCTCCGTGTGAGGGCAAGCGCGCG 432
QY 1670 CCAGGCCCAAGGTGGCGACACCGCCCGCCCATGGCGCGTGGCGCGACCAACCCCT 1729
DB 433 CCAGGCCCAAGGTGGCGACACCGCCCGCCCATGGCGCGTGGCGCGACCAACCCCT 492
QY 1730 CGGCGCCCTCGCGCGCGCGCCACCCCAAGGTGACCACTACAGCCCGCCCTGCGCG 1789
DB 493 CGGCGCCCTCGCGCGCGCGCCACCCCAAGGTGACCACTACAGCCCGCCCTGCGCG 552
QY 1790 CCAGCCCAAGGCCCAAGACCGCTGAGCTCAAGTGGCGGCTGAGCGCTCCACCACTCGA 1849
DB 553 CCAGCCCAAGGCCCAAGACCGCTGAGCTCAAGTGGCGGCTGAGCGCTCCACCACTCGA 612
QY 1850 CCTGGAGAACGGCGCTGCTCCAAACGGCAACGGCAACGGTGTGCGCTCCAAAGACCT 1909
DB 613 CCTGGAGAACGGCGCTGCTCCAAACGGCAACGGCAACGGTGTGCGCTCCAAAGACCT 672
QY 1910 CGGTGCAAGCCCTGCTCCGCGCGCCACCCGCAAGTCCGCC 1953
|||||
```

DB 673 CGGCTGCCAAGCCCTGGTCTCGCGCGCACCGCAAGTCCGCC 716

RESULT 2

AA63355

ID AAX63355 standard; cDNA; 2267 BP.

XX AC AAX63355;

XX XX

XX 16-JUL-1999 (first entry)

XX DE

XX Granule bound starch synthase encoding cDNA.

XX KW

Maize; corn; Zea mays; Delta-9 desaturase; GBSS; target; substrate;

granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;

modulation; gene expression; transgenic plant; cleavage; canola plant;

caffeine synthesis; coffee plant; nicotine production; tobacco;

fruit ripening; flower pigmentation; lignin production; ss.

XX OS

Zea mays.

XX PN

WO9710328-A2.

XX PD

20-MAR-1997.

XX PF

12-JUL-1996; 96WO-US11689.

XX PR

13-JUL-1995; 95US-0001135.

XX PA

(DOWC) DOWELANCO.

XX PI

(RIBO-) RIBOZYME PHARM INC.

XX PT

Edington BE, Folkerts O, Guo L, McSwiggen JA, Merlo DJ;

Merlo PAO, Skokut TA, Young SA, Zwick MG;

XX PS

WPI; 1997-202224/18.

XX PT

Ribozyme which modulates plant gene expression - preferably

modulates expression of DELTA-9 desaturase or granule bound starch

synthase in maize or canola

XX PS

Example 9; Page 31-33; 155pp; English.

XX CC

The present invention describes an enzymatic nucleic acid molecule (I)

with RNA cleaving activity, which modulates the expression of a plant

gene. Also described is a gene comprising a cDNA sequence encoding maize

Delta-9 desaturase. (I) can be used to modulate expression of a gene,

preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)

gene, in a plant (preferably a maize or canola plant). (I) can be used

to modulate caffeine synthesis in a coffee plant, nicotine production in

a tobacco plant, fruit ripening processes in an apple, tomato, pear,

plum or peach plant, flower pigmentation in a rose, petunia,

chrysanthemum or marigold plant or lignin production in a tobacco,

aspen, poplar or pine plant.

XX SQ

Sequence 2267 BP; 465 A; 699 C; 733 G; 370 T; 0 other;

Query Match 24.4%; Score 475.8; DB 18; Length 2267;

Best Local Similarity 59.9%; Pred. No. 4.1e-60;

Matches 979; Conservative 0; Mismatches 557; Indels 99; Gaps 7;

QY 5 TGGACATCGTATGGTGTGCTGAGTTCGCCCCCTTGGTCCAAAGCGGGCGCTGGCG 64

DB 418 TGAACGTCGCTTTCGTCGGCCGAGATGGCGCGTGGAGCAAGACCGGCGCTCGCG 477

QY 65 ATGTGACTGTGTGCTGCTATTGAGTTCAGCGCGGCGGCTCATGACCAATTG 124

DB 478 ACGTCTCGCGGCTGCGCCGCGCATGGCCGGAATGGCACCGTCTCATGTGCTCT 537

QY 125 CCCCTCGCTACGACAGTACGCTGACGCGCTGGGACACCTCGGTGGTGTGACATF 179

DB 538 CTCCCCGCTACGACCAAGTACAAAGGACGCTGGGACACCAGCGCTGTGTCGAGATCAAGA 597

Qy	180	-----CATGGCGAAGAGTCCGCTACTTCCACTTCCATCAAGAAGCGGTGACCGCG	233
Db	598	TGGAGACAGTATCGAGACGCTCAGGTTCTTCCACTTGCTACAAGCGGAGTGGACCGCG	657
Qy	233	TGTGGATTGACCAACCCCTGTTTCTTGCCCAAGAGTGTGGGGCAAGACCGGCTCCAAAGCTGT	292
Db	658	TGTTCTGTTGACCAACCCACTGTTCTTGAGAGGGTTTGGGAAAGACCGAGGAGAAGATCT	717
Qy	293	ACGGCCCCCGCTCGGCGCTGACTACTCGACAACCAACAAGCGTTCGCCCTGTTCTGCA	352
Db	718	ACGGCCTGACGTGGNACGGACTACAGGACACACGCTGCGGTTCAGCTTGCCTGATGG	777
Qy	353	AGGCGCTATTGAGGTGCGCGGTGCTGCCCTTCGGC-----	390
Db	778	AGGAGACACTGAAGTCCAAAGATCCTGAGCCTCAACAACAACCCATACTTCTCCGGAC	837
Qy	391	--CCGCGGAGGACTGGGTCTTGTTGGCCAAAGACTGSCACTCGCCCTGTGCGCGTCC	448
Db	838	CATACGGGGAGGACGTGTTGTTCTGCAAGAGTGGCACACCGGCCCTCTCTGTTGCT	897
Qy	449	TGCTAAGAGCAGTAGTACCAAGCCCAAGGGCCAGTTCACCAAGGCCAAAGTCGTGCTGGCTA	508
Db	898	ACCTCAAGAGCAACTACCAAGTCCCAGGCACTACAGGACGCAAGACCGCTTTCGTGCA	957
Qy	509	TCCACAACATCGCTTCCAGGGCGCGATGTGGAGGAGGCTTTCGAAGGACACGAAGTGC	568
Db	958	TCCACAACATCTCTACCAAGGCGGGTTCGCCCTTCTCCGACTACCCGAGCTGAACCTCC	1017
Qy	569	CCAGAGCGCGTTTGACAAGCTGGGCTTCTCGAGCGGTATGCCAAGGTTTACACTGAGG	628
Db	1018	CGNAGAGATTCAGTCTGCTTCGATTTTCATCGACGGCTACGAGAAG-----	1064
Qy	629	CCACCCCCATGAGGAGGACGAGAAGCCGCCCTGACGGGAAAGACCTACAAGAAGATCA	688
Db	1065	-----CCCGTGGAA-----GCGCGGAAGATCA	1086
Qy	689	ACTGGCTGAAGGTGGCATATTGCGCGCGGACAGCTGGTGACTGTGTGCCCCAACTACG	748
Db	1087	ACTGGATGAAGCGCGGATCTCTCGAGGGCGCAGAGGTCTCTACCGTCAAGCCCTACTACG	1146
Qy	749	CGACCGAGATCGCTGCCGATGCGCGCGGGGTGGAGCTGGACACCGTATCCGCGCCA	808
Db	1147	CCGAGAGCTCATCTCCGCATCGCCAGGGGTGCGAGCTCGACAACATCAIGCGCTCA	1206
Qy	809	AGGGCATGAGGGCAFTGTGAACGGCATGGACATTGAGAGTGGAAACCCCAAGACCGACA	868
Db	1207	CCGGCATACCGGCATCGTCAACGGCATGGAGCTCAGCGAGTGGGACCCAGCAGGAGCA	1266
Qy	869	AGTTCTGTCTGGCCCTACGACACAGACAGGTTCTAGCGCGCAAGCGCGCGCCCAAGG	928
Db	1267	AGTACATCGCCGTGAAGTACGACGTGTGACGGCGGTGGAGGCCCAAGGCGTGAACAAGG	1326
Qy	929	AGGCCCTGACGCGAGCTGGCGCTCGCTGTGGACCCCGCCCGCCCTGTGCGCCCTCA	988
Db	1327	AGCGCTGACGGGAGGTTCGGGCTCCCGTGGACCGGAACATCCCGTGTGGCGGTTC	1386
Qy	989	TGCGCGCCTGAGGAGCAGAGAGGTGTGGACATCATCTTGGCGCGCCCTGCCCAAGATCC	1048
Db	1387	TCGGCAGGCTGGAAGACAGAGAAGGACCCCGAGTTCATGGCGCGCCCATCCCGCAGCTCA	1446
Qy	1049	TGCGCAACCCCAAG--GTGCAAGATCGCCATCTCTGGGTACCGGCAAGCGCGCTACGAGA	1105
Db	1447	TGGAGATGTGGAGACGTGTCAGATCTGTTCTGTGGCAGCGGCAAGAAAGTTCGAGC	1506
Qy	1106	AGCTGTGTAACGCATTCGSCACCAAGTACAAGGGCGCGGCCCAAGGCGTGTCAAGTTCT	1165
Db	1507	GCATGCTCATGCGCCGAGGAGAAGTTCCACAGGCAAGGTGCGCGCGCTGTCAAGTTC	1566
Qy	1166	CGCGCGCCCTGCGCACATGCTACCGCGCGCGCGCTTTCATGCTGTGTCCTCGCGCT	1225
Db	1567	ACGCGCGCTGCGCACCATCATATGCGCGCGCGGAGTCTCGCGCTCACACGCGCT	1626
Qy	1226	TGAGCCCTTGGCGCTGATCCAGTGCAGGCCATGSCACTACGGTACCGTGCCTCGGTAG	1285

[illegible]

PN WO9814601-A1.
 XX 09-APR-1998.
 XX PF 30-SEP-1997; 97WO-US17555.
 XX PR 30-SEP-1996; 96US-0026855.
 XX PA (EXSE-) EXSEED GENETICS LLC.
 XX PI Guan H, Keeling P;
 XX WPI: 1998-240100/21.
 XX DR P-PSDB; AAW56485.
 XX PT Hybrid polypeptide comprising starch-encapsulating region and
 XX protein - useful for, e.g. producing protein(s) resistant to
 XX degradation by stomach acids
 XX Example 2; Page 32-34; 156pp; English.
 CC The sequence is that of the waxy gene which codes for starch
 CC synthase. It can be used in the production of a hybrid
 CC polypeptide comprising a starch-encapsulating region (SER) fused
 CC to a payload protein. The hybrid polypeptide can be used to make
 CC modified starches comprising the payload protein, selected from,
 CC e.g. hormones, growth factors, antibodies, enzymes, dyes,
 CC immunoglobulins, etc. The modified starch can also be used
 CC to provide grain feeds enriched in amino acids. By encapsulating
 CC the payload protein in starch, it is more resistant to
 CC degradation by stomach acids.
 XX SQ Sequence 2542 BP; 510 A; 565 C; 593 G; 574 T; 0 other;

Query Match 22.98; Score 447.4; DB 19; Length 2542;
 Best Local Similarity 58.6%; Pred. No. 4.8e-56;
 Matches 930; Conservative 0; Mismatches 561; Indels 96; Gaps 5;

QY 5 TGGACATCGTCATGTTGCTGCTCAGTTCGCCCTTGGTCCAAAGCGGCGGCGCTGGGCG 64
 DB 700 TGAACGTGCTGTTGCTGCGGCGCGAGATGGCCCTGGAGCAAGACGCGGCGCTCGGTTG 759
 QY 65 ATGTGACTGTGGTGGCTGCTATTGAGCTGGTCAAGCGCGGCGCGGCTGATGACCATG 124
 DB 760 ACGTCCTGGTGGCTGCTCCCTCCATGGCTGCGATGGCCAGGTCATGTTGATCT 819
 QY 125 CCCTCCCTAGACCACTAGCTGACGCTGCGGACACCTGGTGGTGGTGGTGGTGGTGGTGG 184
 DB 820 CTCCTCGGTACGACAGTACAAAGCAAGCTGGGATACCAAGGTTGTGGCTGAGATCAAG 879
 QY 185 -----GCGAAGGTCGCTTACTTCCACTCCATCAAGAGGCGGTGCAACCGG 232
 DB 880 TTGAGACAGTACGAGAGGTGAGGTTTTCATTCTACAAAGCTGGAGTGCACCGTG 939
 QY 233 TGTGGATTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 292
 DB 940 TGTTCATCGACATCCGCTCATCTCTGAGAGGTTTGGGAAAGACCGGTCGAGAAATCT 999
 QY 293 ACGGCCCCGCTCCGGGCTGACTTACTTGGACCAACCAAGCGCTTCGCCCTGTCTGCA 352
 DB 1000 ACGGACCTGACACTGGAGTTGATTACAAAGACCAACCAAGATGCGTTTCAGCCTCTTTGCC 1059
 QY 353 AGGCGGCTATTGAGGCTGCGCGGTGCTGCCCTTCGGGCCCC----- 393
 DB 1060 AGGACGACTCGAGGCTTCCTAGGATCTTAACCTCAACCAACCAACCTACTTCAAGGAA 1119
 QY 394 -----GCGAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
 DB 1120 CTATGCTGAGGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1179
 QY 449 TGTGAGGACGAGTACCAAGCCCAAGGCGGAGTTTCAACAAAGGCAAGCTCGGTGCTGCTA 508
 DB 1180 ACCTGAAGAACAACTACCAACCCCAATGGCATCTACAGGAATGCAAGGTTGCTTCTGCA 1239

QY 509 TCACACATCGCTTCCAGGCGCGCATGTGGAGGAGGCTTTCAGGACACAGCAAGCTGC 568
 DB 1240 TCACACATCTCTTACCAGGCGCGTTTCGCTTTCGAGGATTACCTGAGCTGAACTCT 1299
 QY 569 CCAGGCGGCTTTCACAAAGCTGGCTTCTCGAGCGGTATGCCAAGGTTTACACTGAGG 628
 DB 1300 CCGAGAGGTTTCAAGTCACTCTTCGATTTCATCGAGGGTATGAC----- 1343
 QY 629 CCACCCCATGAGGAGGAGGAGAGAGCCCGCTGACCGGAAAGACCTTACAGAGATCA 588
 DB 1344 -----ACGCGGTGAGGAGGAGAGATCA 1368
 QY 689 ACTGGCTGAAGGTGGCAATTATCGCCGCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
 DB 1369 ACTGGATGAAGCGCGAATCTTGAAGCGGACAGGCTGCTACCGTGAAGCGGCTACTAG 1428
 QY 749 CGACCGAGATCGTCCGATGCGCGGCGGCTGTGGAGTGACACCGCTATCCCGCGCA 808
 DB 1429 CCGAGGAGCTCATCTCCGCGCATCGCCAGGGATCGCACAACTCATGCGGCTCA 1488
 QY 809 AGGCAATTGAGGCGCATCTGAACGCGCATGGACATTCAGAGTGGAACCCCAAGACCGACA 868
 DB 1489 CCGCATCACCGCATCTCTCAAGCGCATGGCTCAGCGAGTGGGATCTTAGCAAGGACA 1548
 QY 869 AGTTCTGCTGTGGCGCTTACGACCAAGACAGCGTCTACCGCGGCAAGCGCGCGCAAG 928
 DB 1549 AGTACATCACCGCAAGTACGACGCAACCGGCAATCAGGCGAAGCGCTGAACAAG 1608
 QY 929 AGGCGCTGAGGCGGCTGGCGCTGTGTGGACCCACCGCCCTCTGTTGCGCTTCA 988
 DB 1609 AGGCGTTGAGGCGGAGCGGCTTTCGCTGCGACAGAAATCCCACTGATCGCGTTCA 1668
 QY 989 TCGCGCGCTGAGGAGGAGGAGGCTGTGGACATCATCTGCGCGCTGCTGCGCAAGATCC 1048
 DB 1669 TCGCGAGCTGAGGAGGAGGAGGCGCTGAGCTATGCGCGCGCTGCTGCGGAGCTCA 1728
 QY 1049 TGGCCACCCCAAGGTGAGATGCGCATCTCTGGGTACCGGCAAGCGCGCTACGAGAGC 1108
 DB 1729 TG----CAGGAGGAGCTCCAGATCGTTCTCTGGGTACTGGAAGAAAGTTCGAGAAGC 1785
 QY 1109 TGTGAACGCCATCGGACCAAGTACAGGCGCGCGCGCAAGGCGGTGTCAGTCTCGG 1168
 DB 1786 TGCTCAAGAGCATGAGGAGAGATTCGCGGCAAGGTGAGGCGGTGTTGAAGTTCAAG 1845
 QY 1169 CGCCCTGGCGCATGCTCACCGCGCGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1228
 DB 1846 CGCGCTGCTCATCTCATATGCGCGGAGCGAGCTGCTGCGCTGCCAGCGCTTCG 1905
 QY 1229 AGCCCTGGCGCTGATCCAGCTGCACGCCATGCACTACGGTACCGTGCCTGCTGCTGCTG 1288
 DB 1906 AGCCCTGTGACTCATCCAGTGCAGGGATGAGATACGGAACGCGCTGTGCTGCGGT 1965
 QY 1289 CCAGCGGCGCTGCTGACACCGCTCAAGAGGCGCTCACCGCTTCCACATGCGCGGCC 1348
 DB 1966 CCACCGGTGGCTGCTGGACACGCTCATCGAAGGCAAGACTGGTTTCCACATGCGCGCTC 2025
 QY 1349 TGAACCCCGAC-----AAGCTGGAGGAGGCTGACGCGCGCGCTGCGCGCGCGCTGCG 1402
 DB 2026 TCACGCTGCACTGCAAGGTGCTGGAGCCACGAGCTGAAGAGTGGCGGCGCCCTGA 2085
 QY 1403 GCGCTGCCAGGAGTGTTCGCGGCGCGCGCTACCCCGAGATGGTGGCGCAACTGCATCA 1462
 DB 2086 AGCGCGCATCAAGGCTGCTGGCACGCGCGGTACGAGGAGATGTCAGGAACTGCAIGA 2145
 QY 1463 GCGAGGAGCTGCTCTGTTCCAGCCCGCGCGAGAGTGGAGGCGCTGCTGGAGAGGTTG 1522
 DB 2146 ACCAGGAGCTCTCTCTGGAAGGCGCTGCGAAGAACTGGGAGATGTGCTCTGCGCGCTG 2205
 QY 1523 TGTACGGAAGGCGGCTGCGCACCG 1549
 DB 2206 GGTGCGCGGAGCGCGCGCGGAGTCG 2232

```

RESULT 5
ABK53210
ID ABK53210 standard; DNA; 2161 BP.
XX AC ABK53210;
XX DT 14-AUG-2002 (first entry)
XX DE Potato granule-bound starch synthase I (GBSSI) DNA sequence.
XX KW Starch; amylose; cereal crop; commodity starch; thickened foodstuff;
XX LW bread; baking; pasta; potato; granule-bound starch synthase I; GBSSI; ds.
XX OS Solanum tuberosum.
XX PN W0200218606-A1.
XX PD 07-MAR-2002.
XX PF 28-AUG-2000; 2000W0-US23494.
XX PR 28-AUG-2000; 2000W0-US23494.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Broglie K, Lightner J;
XX DR WPI; 2002-404556/43.
XX PT Novel starch isolated from cereal crop with a modification of amylose
XX content and/or amylose weight distribution relative to commodity starch
XX from same species of the cereal crop, for preparing thickened
XX foodstuffs.
XX Example 1; Page 36; 44pp; English.
XX CC The present invention relates to a new starch comprising amylose,
XX where the starch is isolated from a cereal crop, and comprises a 50%
XX increase in average molecular weight relative to commodity starch from
XX the same species of the cereal crop from which starch was isolated.
XX The starch of the invention is useful for preparing thickened foodstuffs
XX by combining the starch, a foodstuff and water and cooking the resulting
XX composition as necessary to produce a thickened foodstuff. The invention
XX is also useful for preparing foodstuffs such as breads, baked goods,
XX pastas, etc. The present nucleic acid sequence represents the potato
XX granule-bound starch synthase I (GBSSI) DNA sequence that was used in
XX the methods of the invention for generation of a potato full-length
XX sense GBSSI DNA construct.
XX SQ Sequence 2161 BP; 614 A; 428 C; 505 G; 614 T; 0 other;

Query Match 16.2%; Score 316.8; DB 24; Length 2161;
Best Local Similarity 53.8%; Pred. No. 2.6e-37;
Matches 836; Conservative 0; Mismatches 622; Indels 96; Gaps 5;

QY 5 TGGACATCGTGAGGTGCTGTGAGTGCAGTCCGCTTGGTCCAGACGGGGCGCTGGGCG 64
DB 278 TGAACCTTGATCTTGTGGGTACTGAGGTGGTCTCTGGGCAAAACCTGGTGGACTAGGTG 337
QY 65 ATGTGACTGTGGCTGCCTATTGAGTGTCTGAGCGCGGCCCGGCTCATGACCATTTG 124
DB 338 ATGTTCTTGTGGTACTACCAACAGCCCTTGCAGCCCGGACATCGGGTAAATGACAATAT 397
QY 125 CCCCTCCTACGACAGTACGCTGACGCTGGGACACCTCGGTGGTGGTGGACATCATGG 184
DB 398 CCCCCCGTTATGACCAATACAAAGATGCTTGGGATACTAGGTTGCGGTTGAGTCAAAG 457
QY 185 -----GGCAGAGTTCGGTACTTCCACTCCATCAAGAGGGGTGCACCGCG 232
DB 458 TTGGAGACAGCATTTGAAATTTGCTGTTCTTCACTCTATAAAGCTGGGGTTGATCGTG 517
QY 233 TGTGGATTGACCAACCCCTCGTCTTCTGCGCAAGGTCTTGGGCAAGACCGGCTCCCAAGCTGT 292

```

Db 1544 CGACTGGTGACTTGTTCACACTGTGAAGAGGCTACTACTGATTCATATGGAGCCT 1603
QY 1349 TGA-----ACCCGACAAGCTGACGAGGCTGACGCGCCCTGCCCGCCACCGTGC 1402
Db 1604 TCAATGTTGAATGGCATGTTGTCACCCAGCTGATGCTTTAAGATAGTAAACAACAGTTG 1663
QY 1403 GCCGTGCCAGGAGGTGTTTCGGGGCGGCCCTACCCCGAGATGGTGGCCCACTGCATCA 1462
Db 1664 CTAGAGCTTGTGAGCTATGCGACCCCTCGCATTTGCTGATGATGATAAAAAATGTCATGT 1723
QY 1463 GCCAGGACCTCTCTGTTGCCAAGCCGCCAGAGTGGGAGGCGCTGCTGGAGG 1516
Db 1724 CAGAGGAACCTCTCTGGAAGCACTGCCAGAATGGAGACATTTGCTATGG 1777

RESULT 6
AAC32824
ID AAC32824 standard; DNA; 2115 BP.
XX AC AAC32824;
XX AC
XX AC
DT 17-OCT-2000 (first entry)
XX AC
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 779.
XX DE
XX Arabidopsis thaliana. Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.

Best Local Similarity 53.7%; Prd. No. 1.3e-34;	
Matches	820; Conservative 0; Mismatches 610; Indels 96; Gaps
QY	20 TTGCTGTGAGTGGCCCTTGGTCCAAAGCGCGCGCTGGGCGATGACCTGGTGGCC 79
Db	
QY	415 TTGGAGCTGAAGTTGGTCCATGGAGTAAACTGGTGGCTTGGTGGATTTCTCGGTGGC 474
Db	
QY	80 TGCCTATTGAGCTGCTCAAGCGCGCCACCGCGCTCATGACCAATGGCCCTCGCTAGCACC 139
Db	
QY	475 TACCTCCAGCTCTTGGTCTAGAGCGCCACCGTGTGATGACAAATGCTCTCGTATGACC 534
Db	
QY	140 AGTAGCTGAGCCTCGGACACCTCGGTGGTGGTGGGATC-----ATGGCGG 187
Db	
QY	535 AATATAAGATGCTGGGACACTTGTCTGTGGTTCAGATCAAGTTGGGATTAAGTTG 594
Db	
QY	188 AGAAGGTCGCTACTTCCACTCCATCAAGAGGCGTGCACCGGTGTGATTTGACCAACC 247
Db	
QY	595 AGAATGTCGTTCTTCATTCACAAACAGAGGATGTGCTGTTGTTGTTGATCATC 654
Db	
QY	248 CCTGTTCTCGGCAAGTCTGGGGCAAGACCGGCTCCAAAGTGTAGGCGCCCGCTCGG 307
Db	
QY	655 CAATCTTCTTGTGAAGTTTGGGCAACACAGGATCCAAATCTATGTTCTATAACTG 714
Db	
QY	308 GCGTGACTACTGGACAAACAGGCGTTCGCCCTGTCTCAAGGCGCGCTATTGAGG 367
Db	
QY	715 GAGTAGACTACAATGACAACTCGGTTTCAGTTTGTGTCAGGCTGCTCTTGAGG 774
Db	
QY	368 CTGCGCGGCTGCTCGCTTGGCGCGCGGAGGATCG----- 405
Db	
QY	775 CACCAGGTTCTGAACCTGAACAGCAGAGTACTTCTCTGGAACATATGTTGAAGTG 834
Db	
QY	406 --GTCTTGTGGCCACGACTGGCGACTCCGCGCTGGTGGCGCTCTGCTGAAGGAGAGT 463
Db	
QY	835 TAGTCTTGTGGCAATGACTGGCACACTGCTCTACTTCCATGTTACTTCAATCTATGT 894
Db	
QY	464 ACCAGCCCAAGGCGAGTTACCAAGGCGAAGTGGTGGCTATCCACCAATCGCCT 523
Db	
QY	895 ATCAATCCCGCGGAGTCTACATGAATGCAAGGTGGTCTTCTGCAATTCACCAATAGCCT 954
Db	
QY	524 TCCAGGCGCGATGCGGAGGAGGCTTCAAGGACAGAGTGCCTCCCGCGCGCTTGG 583
Db	
QY	955 ACCAGGAGAGT----- 975
Db	
QY	584 ACAAGCTGGCTTCTCGGAGGCTATGCCAAGSTTTACATGAGGCGCCCATGAGG 643
Db	
QY	976 ATGACTATTCCCTTCTCAACTTGGCCATCAGCTTTAAAGTTCTTTGACTTTCATGACG 1035
Db	
QY	644 AGGAGGAGAGCCCGCTGACGGGAAGACCTACAGAGATCACTGCTCAAGGCTG 703
Db	
QY	1036 GGTATGAAAGCC-----AGTAAAGGACGGAATAAATGATGATGAAGGCTG 1083
Db	
QY	704 GCATTATCGCGCGCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
Db	
QY	1084 CAATTCGGAAGCTCACCGTGTCTTAAGATTAGTTCATCTGCTCAAGACTCATCT 1143
Db	
QY	764 CCGATGCGCGCGGCTGTGGAGCTGGACACCGCTCATCCGCGCAAGGCGCTTGAAGGCA 823
Db	
QY	1144 CTGGAGTTGATAGAGGCTGGAATTGCATAAATCTTCAATGAAACAGTTTCCGGA 1203
Db	
QY	824 TTGTGAGGCGATGGCAATTGAGAGTGGAAACCCAGACCGACAGTCTCTCTGCGC 883
Db	
QY	1204 TTATTAATGGAATGGATGTTCAAGATGGAACCGCTACTGCAAGTACATCATCA 1263
Db	
QY	884 CTTACGACCAAGACGCTCTACCGCGGAGGCGCGCGCGAGGCGCTTCAGGCGG 943
Db	
QY	1264 AATACGATTATACCCTGTTACAGATGCTAAACCATTTGATCAAGAGACTTTCAGGCTG 1323
Db	
QY	944 AGCTGGGCTGCTGTGGACCCCGCGCGCGCTGTTGCTGCTTCTATCGGCGCTGAGG 1003
Db	
QY	1324 CTGTTGACTTCCGCTGGACAGGATGTCGGGTATCCGTTTCTATAGAGGATTTGAGG 1383
Db	
QY	1004 AGCAGAGGTTGGACATCATCTGCGCGCGCTGCCAAGATCTGCTGCGCACCCCAAGG 1063
Db	

Query Match

15.3%; DB 21; Length 2115;

Score 298; DB 21; Length 2115;

Db 1384 AGCAGAGGGTCTGATATTCTAGTGAAGCTATTTCCAAAGTTCATGG---GGCTCAATG 1440
QY 1064 TGCAGATCGCCATCTCTGGTACCGGCAAGCGCGCTACGAGAGCTGGTGAAGCGCATCG 1123
Db 1441 TTCAGATGGTTATCTCTGGGACTTGGAAAGAAAGATGGAGGCTCAGATCTTTGAAGTAG 1500
QY 1124 GCACCAAGTACAAGGCGCGCCCAAGGGCTGTCAAGTTCTCGGCGCCCTGGCGCACA 1183
Db 1501 AAGAGAGATTCCAGGAAGCGGTTGGAGTGGCGAAATTCACGTGCCATTGGCTCATA 1560
QY 1184 TGTCTACCGCGCGCGGCTACGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1243
Db 1561 TGATCACTGTGTGAGCTGACTTTCATCATCTTCCCAAGCAGGTTGAGCGGTGGTCTCA 1620
QY 1244 TCCAGCTGCAGCCATGCACTACGTACCTGACCGTGGTGGTGGTGGTGGTGGTGGTGG 1303
Db 1621 TCCAGCTGCAGCCATGCACTACGTACCTGACCGTGGTGGTGGTGGTGGTGGTGGTGG 1680
QY 1304 TCCACACCGTCAAGGAGGGGCTCACCAGGCTTCCACATGGG-----CGCCCTGAACCCCG 1357
Db 1681 TGGACACTGTGAAGATGGCTACACAGGTTTCCACATTTGAAGATTCAACGTCAGGTG 1740
QY 1358 ACAAGTGGACGAGGCTGACGCGGACGCGCTGCGCGCCAGCTGCGCGCTGCGCGGAGG 1417
Db 1741 AAGTTGGATCCAGATGATGTGATACACACGCAAGAGGCTGTGACAAGAGCCGTTGCG 1800
QY 1418 TGTTCGGGCGCGCTACCGCGAGATGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 1477
Db 1801 TATATGGAACATCCGCAATGCAAGAAATGGTCAAGAACTGATGCAAGAACTGATGCAAG 1860
QY 1478 GTTCCAAAGCGCGCCCAAGATGGGAG 1503
Db 1861 GGAAGGACCTGGAGGTTGGGAG 1886

RESULT 7
ABK53215
ID ABK53215 standard; cDNA; 2183 bp.
XX
AC ABK53215;
XX
DT 14-AUG-2002 (first entry)
XX
DE Canna edulis granule-bound starch synthase I (GBSSI) cDNA sequence.
XX
KW Starch; amylose; cereal crop; commodity starch; thickened foodstuff;
KW bread; baking; pasta; potato; granule-bound starch synthase I; GBSSI; ss.
OS Canna edulis.
XX
PN WO200218606-A1.
XX
PD 07-MAR-2002.
XX
PF 28-AUG-2000; 2000WO-US23494.
XX
PR 28-AUG-2000; 2000WO-US23494.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Broglie K, Lightner J;
XX
DR WP1; 2002-404556/43.
XX
PT Novel starch isolated from cereal crop with a modification of amylose
PT content and/or amylose weight distribution relative to commodity starch
PT from same species of the cereal crop, for preparing thickened
PT foodstuffs.
XX
PS Example 1; Page 37-38; 44pp; English.
XX
CC The present invention relates to a new starch comprising amylose,
CC where the starch is isolated from a cereal crop, and comprises a 50%

CC increase in average molecular weight relative to commodity starch from
CC the same species of the cereal crop from which starch was isolated.
CC The starch of the invention is useful for preparing thickened foodstuffs
CC by combining the starch, a foodstuff and water and cooking the resulting
CC composition as necessary to produce a thickened foodstuff. The invention
CC is also useful for preparing foodstuffs such as breads, baked goods,
CC pastas, etc. The present nucleic acid sequence represents the Canna
CC edulis granule-bound starch synthase I (GBSSI) cDNA sequence in clone
CC etlc.pk007.015 that was used in the methods of the invention for
CC generation of a full-length sense Canna edulis GBSSI construct.

XX
SQ Sequence 2183 bp; 636 A; 428 C; 516 G; 603 T; 0 other;

Query Match 13.2%; Score 258; DB 24; Length 2183;
Best Local Similarity 51.6%; Pred. No. 7.2e-29;
Matches 794; Conservative 0; Mismatches 650; Indels 96; Gaps 5;

QY 5 TGGNATCGTATGTTGCTGCTGAGGTGGCCCTTGGTCCAAAGCGGGGCTGGGCG 64
Db 357 TGAACTTGGGGTTTGGTTGTGAGGTAGCTCCATGGAGCAAACTGGGGCTTGGCG 416
QY 65 ATGTGACTGTGGCTGCTGCTATTGAGCTGFTCAAGCGCGCCACCGCTCATGACCAT 124
Db 417 ATGTTCTTATAGATTGCCACCTGCTATGCTGCAATTTGGCACAGGGTCATGACCG 476
QY 125 CCGCTGCTAGCAGCAGTACGCTGACGCTTGGGACACCTCGTGGTGGTGGACAT---- 179
Db 477 CGCACGATATGACCAATATAAAGATATCTGGGATACAAGTGTCCAGTTGAGTAAAG 536
QY 180 -----CATGGGCGAGAAGTCCGCTACTTCCACTCCATCAAGAGGGGTGACCGCG 232
Db 537 TTGGGATAAGATTGAAACTGTCGGCTTCTTCCACTCTACAAAGGGGAGTTGATCGG 596
QY 233 TGTGGATTGACACCCCTGCTTCTGCGCAAGGTCTGGGCAAGACCGCTTCCAAAGTGT 292
Db 597 TTTTGTGGATACCCCTATGTTCTCGAAGAGTTTGGGGAAACAGAGGAAATAT 656
QY 293 ACGGCCCCCGCTCGGCGCTGACTTACCTGGACACCAAGCGCTTCGCCCTGTCTTTCGA 352
Db 657 ATGCTCCTGTTACAGGAACAGATTATGCAGACAATCACTAAGATTGAGCTTTTGTGC 716
QY 353 AGGCGCTATTGAGGCTGCGCGGTGCTGCGCTTGGCGCCCGGGGAGGATGCG----- 405
Db 717 TGGAGCTTGGAGTCCAAAGACTTCTAAATCTCAACACAGCAATACTATTCTGGAC 776
QY 406 -----GTCTTGTGGCAACGACTGCGCTCGCGCTGCTGCGCTGCTGCGCTGCT 448
Db 777 CATATGGAGATGATGTTGTTTATTTGCCAAGCTTGGCATTTGCTCTACTGCCCTGCT 836
QY 449 TGTGAGGACGAGTACCAAGCCCAAGGCGCATTCACCAAGGCAAGTGGTGGTGGCTA 508
Db 837 ACTTGAACACTATGTACCAATCATGGTATTATACATGAATGCTAAGTTTGCATTTTGA 896
QY 509 TCCACACATCGCTTCCAGGCGCGCATGTGGGAGGAGGCTTTCAAGGACACCAAGCTGC 568
Db 897 TTTCAATATGCTTACAGGCGCGGATTTGCGCTTTTTCGGACTTTGAACCTCTTAATCTCC 956
QY 569 CCGAGCGCGCTTTGACAAGCTGGCCTTCTCGGACGCGCTATGCCAAGGTTTACACTGAG 628
Db 957 CCAATAAATTAAATCTTCATTTGATTTTCATGGATGATGACAACT----- 1006
QY 629 CCACCCCATGGAGGAGGAG 688
Db 1007 -----GTGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1025
QY 689 ACTGGCTGAAGGCTGATTAATTCGCGCGCAGCAAGCTGTGCTGCTGCTGCTGCTGCTG 748
Db 1026 ATTGGATGAAGGCTGGAATAGATAGTGTGCTTGGAGCTTGGAGCTGAGCCCATATATG 1085
QY 749 CGACCGAGATCGCTGCGGATGCGCGGCTGCTGAGGCTGGACACCGTCATCCGCGCCA 808
Db 1086 CCCAAGCTTGTCTCAGGGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1145

QY 809 AGGGCATTGAGGCGATTTGTAACGGCATGGACATTTGAGGAGTGGAAACCCCAAGACCGACA 868
 Db 1146 AAACCATCTGTGGAATAGTAATAGTGAATGGAACACACCGAGTGAATCCATTAAACAGACA 1205
 QY 869 AGTTCTGTCTGGCCCTAGACACCAAGAGAGAGTCTACGCGGCAAGGCGCGCCCAAGG 928
 Db 1206 AATATATTCTCAAACTACGATGCAACAACTGATTTGGATGCAAAACCTCTCTGTAAAGG 1265
 QY 929 AGGCCCTGAGGCGGAGTGGGCTCCCTGTGGAGCCCAAGCCGCGCCCTGTTCGCCCTTCA 988
 Db 1266 AAGCTTTGCAAGCTGAGTGGCTCCCTGTTAAACAAAACAAAGCTGTTTGGCCCTTG 1325
 QY 989 TGGGCGCCTGGAGGAGAGAGGTTGGACATATCTTGGCCGCTGGCCCAAGATCC 1048
 Db 1326 TTGGAAGACTAGATGAGCAAGAGGCTCAGACATTTAGTGTGAGCAATTTCCAGAACTTC 1385
 QY 1049 TGGCCACCCCAAGGTCAGATGCCATCTGTGGTACCGGCAAGGCGGCTACGAGAAGC 1108
 Db 1386 T---TTGTGAGATGTTCAAGTGATAGTACTTGGCACTGGCAAGAGAAAGTTGGAGAGTG 1442
 QY 1109 TGGTGAACGCCAPCGGCACCAAGTACAAGGCGCGCCCAAGGCGGTGGTCAAGTTCTCGG 1168
 Db 1443 AACTTACATTTAGTGAAGAAATGTTTCCAGACAAATTCAGAGCACATCTCAAAATTCAAAG 1502
 QY 1169 CGCCCTGGGCGACATGTCACCGCGGCGCGGCGGCTGATGCTGAGTGGCCCTCGCGCTTCG 1228
 Db 1503 TTCTTTAGCTATGCAATCATGCAAGAGTGTGATATCTCTTGTATTTCCAAAGCAGATTCG 1562
 QY 1229 AGCCCTGGCGCGGATCCAGCTGCACGCCATGCATACGCTACCGTACCGTCCGCTGTAGCCCT 1288
 Db 1563 AACCCCTGTGGCCCTCATTCAGCTTCAGGCCATGCGATGGAATCTCCCTATGTGTAGCA 1622
 QY 1289 CCACCGCGCGCTGGTGGACACCGTCAAGGAGGCGGTCAACCGCTTCCACATGGGCGCC- 1347
 Db 1623 CCACCTGTGGACTGTTGACACTGTCAAGAGGCTTCACCTGGCTTCCATATGGGCCCT 1682
 QY 1348 -----CTGAACCCCGCAAGCTGGAGAGGCTGACGCGCGAGCGCTGGCGCGCACCGTGC 1402
 Db 1683 TCAGTGTGGAGTGTGATGCGGTAGACAAAGCTGATGTATACAAAGATTTGCGAAACACGA 1742
 QY 1403 GCGGTGCGACGAGGTGTTTGGCGGCGCGCTACCCGAGATGGTGGCCAACTGCATCA 1462
 Db 1743 AAGGGCCCTCAAGTCTATGGAACACCTGCTTTTGTGGAGATGATCAAGAACTGCAIGA 1802
 QY 1463 GCAGGACCTGTCTGTGTCAAAGCCCGCCCAAGTGGGA 1502
 Db 1803 ACCAAGATCTCTCATGGAAGGACCTGCAAGAGAGTGGGA 1842

RESULT 8

AAC86435

ID AAC86435 standard; cdna; 2807 BP.

XX

AC AAC86435;

XX

DT 01-MAR-2001 (first entry)

XX

DE Wheat starch synthase clone wssIID cdna.

XX

KW Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
 KW food product; adhesive; ss.

XX

OS Triticum aestivum.

XX

PN W0200066745-A1.

XX

PD 09-NOV-2000.

XX

PF 28-APR-2000; 2000WO-AU000385.

XX

PR 29-APR-1999; 99AU-00000052.

XX

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (GOOD-) GOODMAN FIELDER LTD.
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX

PI Morell M, Li Z, Rahman S, Appels R;
 XX WPI; 2000-647602/62.

XX

DR Nucleic acid molecules encoding wheat starch synthase (WST)-I and
 XX WST-II, useful in modifying plant starch content and/or composition -
 PT disclosure; Fig 2; 21pp; English.

XX

PS The present invention relates to novel protein and coding sequences from
 XX wheat. The proteins are wheat starch synthases, designated SSII and
 CC SSIII. These can be used in the modification of plant starch content or
 CC composition, and to screen plants to identify mutations which affect
 CC starch content and composition. The starch can then be used in food
 CC products, such as flour, and in films, coatings, adhesives, building
 CC materials and packaging materials.

XX

SQ Sequence 2807 BP; 549 A; 844 C; 907 G; 507 T; 0 other;
 Query Match 11.3%; Score 221; DB 21; Length 2807;
 Best Local Similarity 56.2%; Pred No. 1.4e-23;
 Matches 485; Conservative 0; Mismatches 360; Indels 18; Gaps 3;

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY 1385 CCCTGGCCGCCACCGTGGCGGTCCAGAGGAGTGTTCGGGGCGGCGGCTACCCCGAGA 1444
 Db 2337 TCGAGCGGCTCGGCACTGCTCCGACCTACCGGACTACAAGGAGAGCTGGAGGGCC 2396
 QY 1445 TGGTGGCAACTGCATCAGCAGGAGCTGCTGCTGCTCCAGCCGCCAGAGTGGGAGG 1504
 Db 2397 TCCAGGAGCGGCGATGTCGAGGACTTCAGTGGGAGCAAGCGCAAGTCTACGAGG 2456
 QY 1505 GCTGCTGTGGAGGAGTGTGTAC 1527
 Db 2457 ACCTCTCTCTCAAGGCCAAGTAC 2479

RESULT 9
 AAC86411
 ID AAC86411 standard; cDNA; 2842 BP.
 AC AAC86411;
 DT 01-MAR-2001 (first entry)
 DE Wheat starch synthase II coding sequence SEQ ID NO: 3.
 KW Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
 KW food product; adhesive; ss.
 XX Triticum aestivum.
 XX WO200066745-A1.
 PN 09-NOV-2000.
 XX 28-APR-2000; 2000WO-AU00385.
 XX 29-APR-1999; 99AU-0000052.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (GOOD-) GOODMAN FIELDER LTD.
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 XX Morell M, Li Z, Rahman S, Appels R;
 PI WPI; 2000-647602/62.
 DR P-PSDB; AAB37567.
 XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and
 PT WST-II, useful in modifying plant starch content and/or composition -
 XX Claim 1; Page 155-158; 211pp; English.
 XX The present invention relates to novel protein and coding sequences from
 CC wheat. The proteins are wheat starch synthases, designated SSII and
 CC SSIII. These can be used in the modification of plant starch content or
 CC composition, and to screen plants to identify mutations which affect
 CC starch content and composition. The starch can then be used in food
 CC products, such as flour, and in films, coatings, adhesives, building
 CC materials and packaging materials.
 XX Sequence 2842 BP; 561 A; 851 C; 919 G; 511 T; 0 other;

Query Match 11.3%; Score 221; DB 21; Length 2842;
 Best Local Similarity 56.2%; Pred. No. 1.4e-23;
 Matches 485; Conservative 0; Mismatches 360; Indels 18; Gaps 3;

QY 680 AGAAGATCAACTGGCTGAAGGGTGGCATATCGCCCGCAGAGCTGGTGTGTCG 739
 Db 1620 AGCACCCCAACTACTTCGCGCGCGGCTGAGATGCGGACCAAGTGTGCTGGTGAGCC 1679
 QY 740 CCAACTACCGGACCGAGATGCTGCCGATGCCCGCGGCTGTGGAGCTGGACACCGTCA 799
 Db 1680 CCGGGTACCTGTGGGAGCTCAAGACGCTGGAGGGCGGCTTCACGACATCATC 1739

QY 800 TCC---GCGCCAAGGGCAITGAGGGCAITGACGGCATGGACATTTGAGGAGTGAACCC 856
 Db 1740 GGCAGAACGACTGTAAGAACCCGCGGCATCGTCAAGGGCATCGACACATGAGTGAACCC 1799
 QY 857 CCAAGACCGACAAAGTTCTGTCTCGGCCCTAGACCAAGAACAGCGTCT- 904
 Db 1800 CCGAGGTGGAGTCCACCTCAAGTCGACGGCTACACCAACTTTCCTCCCTGGGGAGCGCTGG 1859
 QY 905 ACGCCGGCAAGCGCCGCCAAGGAGGCCCTGCAGGCGGAGCTGGGCTGCTGTGGAGCC 964
 Db 1860 ACTCGGCAAGCGCAGTGCAGAGAGGCCCTGCAGCGGAGCTGGGCTTGCAGGTCCCGG 1919
 QY 965 CCACCGCCGCCCTGTTCGCCCTTCATCGGCCCTCGGAGGAGCAGAGGGTGTGGACATCA 1024
 Db 1920 CCGACGTGCCGCTGCTCGGCTTCATCGGCCCTCGGAGGAGCGCAGAGGGCGTGGAGATCA 1979
 QY 1025 TCCTGGCGGCCCTGCGCCCAAGATCTTGGCCACCCGCCAAGGTGCATGCCATCTCTGGGTA 1084
 Db 1980 TCGCGGAGCGGCAATGCCCTGGATCGT---AGCCAGGAGCTGACGTGCTATGCTGGGCA 2036
 QY 1085 CCGCAAGGGCGCGCTACGAGAAGCTGGTGAACGCCATCGGCACCAAGTACAAAGGCCGCG 1144
 Db 2037 CCGGCCCGCAGACTGTGAGAGCATGCTCGGCACTTCGACGGGAGGACACACGACAAAG 2096
 QY 1145 CCAAGGGCGTGGTCAAGTTCTCGGCCGCCCTCGCGCACATGCTCACCGCGCGGCCGACT 1204
 Db 2097 TGC CGGGTGGTGGGTTCCTCGCTGCCCTCGGCCACCGGATCACGGCGGCGCGCGAGC 2156
 QY 1205 TCATGCTGTGCTCTCGGCTTCGAGCCCTTCGCGGCTGATCCAGCTGCAGCCCATGCACT 1264
 Db 2157 CGTCTCTCATGCCCCCTCGCGGTTGAGCGCTGCGGGTTTGAACCAAGCTTTACGCCATGCGCT 2216
 QY 1265 ACGTACCGCTGCCGCTGTAGCTCCACCGCGGCGCTGGTTCGACACCGTCAAGGAGGCGG 1324
 Db 2217 AGGCAACGCTCCCGCTGCTGCACGCCCTCGGCGGGGTGAGGACACCGTCCCGCGCTCG 2276
 QY 1325 TCACCGCTTCCACATGGGCGCCCTGAACCCCGCACAAAGCTGGAGAGCTGACGCCGACG 1384
 Db 2277 ACCCTTCAACCACTCCGCGCTCGGTGGAGTTTCGACCGCGCGGAGGCGCACAAAGCTGA 2336
 QY 1385 CCCTGGCGGCCACCGTGGCGGTGCCAGGAGGTGTTTGGGGCGGCGCTACCCCGAGA 1444
 Db 2337 TCGAGGCGCTCGGGCACTGCTCCGACCTACCGGGACTACAAGGAGAGCTGGAGGGGCC 2396
 QY 1445 TGGTGGCAACTGCATCAGCAGGAGCACTGCTCGTCCAGCGCGCCGAGAGTGGGAGG 1504
 Db 2397 TCCAGGAGCGGCGATGTCGAGGACTTCAGTGGGAGCATGCCGCCAAGCTCTACGAGG 2456
 QY 1505 GCTGCTGTGGAGGAGTGTGTAC 1527
 Db 2457 ACCTCTCTCTCAAGGCCAAGTAC 2479

RESULT 10
 AAV01528
 ID AAV01528 standard; cDNA to mRNA; 2826 BP.
 XX AAV01528;
 XX 21-MAY-1998 (first entry)
 DE Wheat granule-bound starch synthase cDNA clone pTASS1.
 KW Starch synthase; wheat; transgenic plant; ss.
 OS Triticum aestivum L. cv. Florida.
 XX Key Location/Qualifiers
 FH 162..2561
 FT CDS /*tag= a
 XX WO9745545-A1.

XX 28-APR-2000; 2000WO-AU00385.
XX 29-APR-1999; 99AU-0000052.
PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX Morell M, Li Z, Rahman S, Appels R;
XX WPI; 2000-647602/62.
DR Nucleic acid molecules encoding wheat starch synthase (WST)-I and
XX WST-II, useful in modifying plant starch content and/or composition -
PS Claim 1; Page 195-200; 21lpp; English.
XX The present invention relates to novel protein and coding sequences from
CC wheat. The proteins are wheat starch synthases, designated SSII and
CC SSIII. These can be used in the modification of plant starch content or
CC composition, and to screen plants to identify mutations which affect
CC starch content and composition. The starch can then be used in food
CC products, such as flour, and in films, coatings, adhesives, building
CC materials and packaging materials.
XX Sequence 9024 BP; 2228 A; 2386 C; 2216 G; 2193 T; 1 other;
Query Match 10.9%; Score 212.4; DB 21; Length 9024;
Best Local Similarity 55.7%; Pred. NO. 2.2e-22;
Matches 477; Conservative 0; Mismatches 361; Indels 18; Gaps 3;
QY 687 CAACCTGGCTGAAGGTGGCATATCCCGCCGACACAGCTGGTACTGTGCGCCCAACTA 746
DB 7392 CAACCTACTTGGCGCGCGCTGAAGATGGCGGACCACTGTGCTGGTGGAGCCCGGGTA 7451
QY 747 CGCGACCGAGATCGCTGCCGATGCCCGCGGCTGGAGCTGGACACGCTCATCC- -G 803
DB 7452 CCGTGTGGAGCTCAAGACGGTGGAGGCGGCTGGGGCTTACGACATCATAGCGCAGAA 7511
QY 804 CGCCAGGGCCATTGAGGCGCATTTGAACGGCATGGAGATGGAGTGGAAACCCCAAGAC 863
DB 7512 CGACTGGAAGACCGCGGCATGCTCAACGGCATCGACATGGATGGAGACCCCGAGGT 7571
QY 864 CGACAAAGTTCTGCTGCCCTTACGACACAGACGCTCT- - - - -ACGCCGG 911
DB 7572 GACGCGCCACCTCAAGTCGGAGGCTACACCACTTCTCCCTGAGGACGCTGGACTCCGG 7631
QY 912 CAAGCGCGCGCCAGGAGCGCTCGAGGCGGAGCTGGCGCTGCTGGACCCACCGC 971
DB 7632 CAAGCGCGAGTCAAGGAGGCGCTCGAGCGGAGCTGGGCTGCGAGTCCGCGCGACGT 7691
QY 972 CCCCCTGTGCGCTTATCGGCGCGCTTGAGGAGCAGAGGCTGTGGACATCATCTGGC 1031
DB 7692 GCGCTGTGCGCTTATCGGCGCGCTTGAGGAGCAGAGGCTGTGGACATCATCGGA 7751
QY 1032 CGCCCTGCGCAAGATCTGGCCACCCCAAGTGCAGATCGCCATCCTGGGTACCGGAA 1091
DB 7752 CGCCATGCTTGGATCGTG- - -AGCAGGACCTGAGCTGGTGTGATGCGGACCGGGG 7808
QY 1092 GCGCCCTTACGAGAGCTGGTGAAGCGCATCGGACCAAGTACAGGGCGCGCCAAAGG 1151
DB 7809 CCACGACCTGGAGAGCATGCTCGGCACTTCAGCGGGAGCACACGAAAGTGGCGGG 7868
QY 1152 CGTGTCAAGTTCTCGGCGCGCTTGCGGACATGCTCAAGCGCGCGGCGGACTTCATGCT 1211
DB 7869 GTGGGTGGGGTTCTCGGCTGCGCTGGCGACCGGATCAGCGCGGGCGGACCGCTCT 7928
QY 1212 GGTGCGCTCGCGCTTCGAGCCCTGCGGCTGATCCAGCTGACGCGCATGACATCGGTAC 1271
DB 7929 CATGCCCTCCCGGTTTCGAGCGCTGGGGCTGAACCAAGCTCTACGCCATGGCTACGGAC 7988
QY 1272 CGTGCCCGTGGTAGCTCCACCGGCGGCTGGTGGACACCGCTCAAGGAGGGGCTACCGG 1331

DB 7989 CGTCCCGCTCGTGACGCGCTTGCGGCTCAGGAGACACCTGCGCGGTTTCGACCCCTT 8048
QY 1332 CTTCCACATGGCGCGCTTGAACCCGACAACTGACGAGAGCTGACGCCGAGCCCTGGC 1391
DB 8049 CAACCACTCCGGGCTCGGGTGGAGCTTCGACCGCGCGGAGCGCACAAAGCTGATCGAGG 8108
QY 1392 CGCCACCGTCCGCGCTGCCAGCGAGGTCTTTTGGGGGCGGCTACCCCGAGATGGTGGC 1451
DB 8109 GCTCGGCACCTGCTCCGACCTACCGAGACTTCAAGGAGAGCTGGAGGGCCCTCCAGGA 8168
QY 1452 CAACCTCATCAGCCAGCAAGCTGCTCTGTGTCACAGCCCGCCAGAGTGGGAGGCTGCT 1511
DB 8169 GCGCGGATGTCGAGGAGCTTCACTGGGAGCACGCGCCCAAGCTCTACGAGGAGCTCT 8228
QY 1512 GGAGGAGGTGGTGTAC 1527
DB 8229 CGTCAAGGCCAAGTAC 8244

Search completed: June 3, 2003, 10:08:08
Job time : 344.834 secs

This Page Blank (uspto)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 09:33:29 ; Search time 1905.46 Seconds

(without alignments)

16599.542 Million cell updates/sec

Title: US-09-980-771a-4

Perfect score: 1953

Sequence: 1 gcgcggacatcgtatgt.....ccgccaccgcgaagtcgcgc 1953

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508.6	26.0	786	12	BF864001
2	476.6	24.4	502	14	BQ814687
3	469.8	24.1	473	10	AV640741
4	457.8	23.4	461	10	AV629488
5	456	23.3	666	13	BM003295
6	454.6	23.3	2147	11	AY109531

7	444.4	22.8	458	10	AV622787
8	400.8	20.5	436	10	AV629117
9	395.6	20.3	511	10	AV394077
10	391.4	20.0	393	10	AV631115
11	385.2	18.7	475	10	AM757933
12	352.6	18.1	367	13	BI727902
13	351.2	18.0	799	12	BF863935
14	337.8	17.3	418	10	AV644765
15	325.8	15.1	506	10	AV643281
16	278.4	14.3	702	14	BQ246353
17	272.8	14.0	560	10	AV628313
18	251.8	12.9	552	10	BE024926
19	250.2	12.8	517	10	AV641583
20	245.6	12.6	726	14	BQ804991
21	244.2	12.5	532	10	AV641989
22	242	12.4	585	14	BQ246366
23	235.8	12.1	513	10	AV631004
24	235.8	12.1	552	10	AV640546
25	234.8	12.0	524	10	AV641724
26	234.2	12.0	500	10	AV642869
27	231.8	11.9	510	10	AV395307
28	230.8	11.8	761	12	RG366176
29	223.8	11.5	540	10	AV642722
30	222.2	11.4	1545	11	AY112448
31	216.6	11.1	773	12	RG351175
32	212	10.9	572	14	BQ245812
33	211.8	10.8	486	10	AV642834
34	211.8	10.8	504	10	AV629198
35	210.8	10.8	502	10	AV644517
36	210.2	10.8	511	10	BE423250
37	209.2	10.7	696	12	RG351920
38	208.8	10.7	495	10	AV642565
39	208.2	10.7	543	14	BQ245428
40	207	10.6	641	14	BQ247154
41	206.8	10.6	522	10	BE423625
42	206.4	10.6	729	12	RG599615
43	200.8	10.3	493	10	AV631838
44	200.2	10.3	2498	11	AY109714
45	200	10.2	631	13	BI531619

ALIGNMENTS

RESULT 1
BF864001 786 bp mRNA linear EST 19-JAN-2001
LOCUS 963048D01.yl C. reinhardtii CC-1690, Stress condition I, normalized
DEFINITION , Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BF864001
VERSION BF864001.1 GI:12254145
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 786)
AUTHORS Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C., Lefebvre, P., McDermott, J. P., Shrager, J., Sliflow, C. and Stern, D.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 3
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
Location/Qualifiers
1. .786
/organism="Chlamydomonas reinhardtii"

```
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II"
/Note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, 1hr
, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT 157 a 282 c 244 g 102 t 1 others
ORIGIN
Query Match 26.0%; Score 508.6; DB 12; Length 786;
Best Local Similarity 95.3%; Pred. No. 2e-77; Mismatches 2; Gaps 2;
Matches 546; Conservative 0; Indels 24; Indels 3; Gaps 2;

QY 1383 CGCCCTGGCGCCACCGTGGCGGTGCGAGCGAGTGTTCGGGGGGCGGCTACCCCGA 1442
Db 95 CCCCCGGGCTGCAGGAATTCGGCACGAGGCGGAGGTGTTCGGGGGGCGGCTACCCCGA 154
QY 1443 GATGTGGGCAACTGATCAGCAGGACCTGTCTGTGTCAGGCCCGCCAGAGTGGGA 1502
Db 155 GATGGTGGCAACTGATCAGCAGGACCTGTCTGTGTCAGGCCCGCCAGAGTGGGA 214
QY 1503 GGCCCTGCTGAGGAGTGTGTACGCAAGGCGGCTGGCCACCGCCAGAGGAGGA 1562
Db 215 GGGCTGCTGGAGAGTGTGTACGCAAGGCGGCTGGCCACCGCCAGAGGAGGA 274
QY 1563 GATCAAGTGGCCGTTGCCGAGAGATGCCCGGCGAGCTGCCCGCGGTGTCTTACGCCCC 1622
Db 275 GATCAAGTGGCCGTTGCCGAGAGATGCCCGGCGAGCTGCCCGCGGTGTCTTACGCCCC 334
QY 1623 CACACCTCAAGCCGTCGCGCTCTGGAGGGCAAGCGGCGCGCCGCCCAAGGT 1682
Db 335 CACACCTCAAGCCGTCGCGCTCTGGAGGGCAAGCGTCCCGCGCGCCGCCCAAGGT 394
QY 1683 CGGCACCAACCGCCCGCCATGGCGGTGGCGGCGGACACCCCTCGGGCCCTCGCC 1742
Db 395 CGGCACCAACCGCCCGCCATGGCGGTGGCGGCGGACACCCCTCGGGCCCTCGCC 454
QY 1743 CGCGCGCGCCACCGCCCAAGGTGACCTACAGCCCGCGCGCTGCCCGCCACCGCAAGCC 1802
Db 455 CGCGCGCGCCACCGCCCAAGGTGACCTACAGCCCGCGCGCTGCCCGCCACCGCAAGCC 514
QY 1803 CAAAGCCGCTGGCTCAAGCTGGCGGTGAGGCTCCACACCTCGACCTCGGAGAACGG 1862
Db 515 CAAAGCCGCTGGCTCAAGCTGGCGGTGAGGCTCCACACCTCGACCTCGGAGAACGG 574
QY 1863 CGCTGCTCCCAAGCGCAACGCGTGTGCGGCTTCCAAAGACCTCGGCTGCCAAGCC 1922
Db 575 CGCTGCTCCCAAGCGC-ACGCGCAAGCTGTCTCGGCTTCCAAAGACCTCGGCTGCCAAGCC 633
QY 1923 CTGGGT--CTTCGCGCGCCACCGCAAGTCCGCC 1953
Db 634 CTGGGTCTTCGCGCGCCACCGCAAGTTCGCC 666

RESULT 2
BQ814687 502 bp mRNA linear EST 01-AUG-2002
LOCUS 1030045B10.y1 C. reinhardtii CC-1690, Deflagellation (normalized),
DEFINITION Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BQ814687
VERSION BQ814687.1 GI:22062228
KEYWORDS
```

Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaeae; Chlamydomonas

1 (bases 1 to 502)

REFERENCE
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre
P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1030
Unpublished (2002)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
Location/Qualifiers
1..502
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Deflagellation
(normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Deflagellation library, constructed by John Davies
and Jeffrey McDermott, combines cDNAs from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by pH shock. PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al., (1996) Genome Research 6: 791-806."
BASE COUNT 79 a 200 c 164 g 59 t
ORIGIN

Query Match 24.4%; Score 476.6; DB 14; Length 502;
Best Local Similarity 98.2%; Pred. No. 5.6e-72;
Matches 482; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1353 CCCCAGCAAGCTGACGAGGCTGACGCGCGCTGCGCCCGCCACCGTGCCTGCGCGCGCGAG 1412
Db 12 CCGTGTGCTGGAGGAGGCTGACGCGCGCTGCGCCCGCCACCGTGCCTGCGCGCGAG 71
QY 1413 CGAGGTGTTGCGGGCGCGCTTACCCCGAGATGTGTGCGCCCACTCATCAGCAGGACCT 1472
Db 72 CGAGGTGTTGCGGGCGCGCTTACCCCGAGATGTGTGCGCCCACTCATCAGCAGGACCT 131
QY 1473 GTCCTGTGTCGAAGCCCGCCAGAGAGTGGAGGGCTGTCTGGAGGAGTGGTGTACGGCAA 1532
Db 132 GTCCTGTGTCGAAGCCCGCCAGAGAGTGGAGGGCTGTCTGGAGGAGTGGTGTACGGCAA 191
QY 1533 GGGCGGCGTGGCCACCGCCCAAGAGGAGGATCAAGTGCCTGCGCGCGCGTGCCTGCGCGAGATCCC 1592
Db 192 GGGCGGCGTGGCCACCGCCCAAGAGGAGGATCAAGTGCCTGCGCGCGCGTGCCTGCGCGAGATCCC 251
QY 1593 CGCGACCTGCGCGCGGTGCTTACGGCCCGCCCAACACCTTGAAGCCGCTGTCCGCTCCGT 1652
Db 252 CGCGACCTGCGCGCGGTGCTTACGGCCCGCCCAACACCTTGAAGCCGCTGTCCGCTCCGT 311
QY 1653 GGAGGGCAACG 1712
Db 312 GGAGGGCAACG 371
QY 1713 GCGGCGCAACACCG 1772
Db 372 GCGGCGCAACACCG 431
QY 1773 CAAAGCCG 1832

```

/db_xref="taxon:3055"
/clone="HCL021f06.r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from cells cultured in a medium with bubbling air containing 5% carbon dioxide"

```

BASE COUNT	76 a	162 c	146 g	89 t
ORIGIN				
Query Match	24.1%;	Score 469.8;	DB 10;	Length 473;
Best Local Similarity	99.6%;	Pred. No. 8.1e-71;		
Matches 471;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	17	TGTTGCTGCTGAGTTCGCGCCCTTGTC	CAAGAGCGGCGCGCTGGGCGATGTGAC	TGGTG 76
Db	1	TGTTGCTGCTGAGTTCGCGCCCTTGTC	CAAGAGCGGCGCTGGGCGATGTGAC	TGGTG 60
QY	77	GCCTGCCTATTGAGCTGGTCAAGCGGGCCACGCGCTCATGACCAT	TGCCCTCGCTACG 136	
Db	61	GCCTGCCTATTGAGCTGGTCAAGCGGGCCACGCGCTCATGACCAT	TGCCCTCGCTACG 120	
QY	137	ACCAGTACGCTGACGCCTGGGACACCTCGTGGTCTGGACATCATGGCGAGAAGSTCC	196	
Db	121	ACCAGTACGCTGACGCCTGGGACACCTCGTGGTCTGGACATCATGGCGAGAAGSTCC	180	
QY	197	GCTACTTCCACTCCATCAAGAGGGCGTGCACGCGTGTGGATTGACCAACCCCTGGTTCC	256	
Db	181	GCTACTTCCACTCCATCAAGAGGGCGTGCACGCGTGTGGATTGACCAACCCCTGGTTCC	240	
QY	257	TGSCCAAGTCTTGGGCGACAGCGGCTCCAAGCTGTACGGCCCCCGCTCCGGCGCTGACT	316	
Db	241	TGSCCAAGTCTTGGGCGACAGCGGCTCCAAGCTGTACGGCCCCCGCTCCGGCGCTGACT	300	
QY	317	ACCTGGACAACACAGCGCTTCGCCCTCTTCTGCAAGGCCGCTATTGAGGCTGCCCGG	376	
Db	301	ACCTGGACAACACAGCGCTTCGCCCTCTTCTGCAAGGCCGCTATTGAGGCTGCCCGG	360	

QY 308 GCGCTGACTACCTGGAGAACCAACAGCGCTGCGCCCTGTCTTTCGAAAGCGCGCTATTGAGG 367
 |||||
 Db 301 GCGCTGACTACCTGGAGAACCAACAGCGCTGCGCCCTGTCTTTCGAAAGCGCGCTATTGAGG 360
 |||||
 QY 368 CTGCCCGCGTGTGCGCTTTCGCGCGCGGAGGACTGCGTCTTCGTGGGCAAGACTGGC 427
 |||||
 Db 361 CTGCCCGCGTGTGCGCTTTCGCGCGCGGAGGACTGCGTCTTCGTGGGCAAGACTGGC 420
 |||||
 QY 428 ACTCCGCGCTGTGCGCGCTTTCGCTGAAGGACGAGTACCAG 468
 |||||
 Db 421 ACTCCGCGCTGTGCGCGCTTTCGCTGAAGGACGAGTACCAG 461
 |||||

RESULT 5
 LOCUS BM003295 666 bp mRNA linear EST 25-OCT-2001
 DEFINITION Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
 ACCESSION BM003295
 VERSION BM003295.1 GI:16438075
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii.
 ORGANISM Chlamydomonas reinhardtii.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadales; Chlamydomonas.
 REFERENCE 1 (bases 1 to 666)
 AUTHORS Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre
 P., McMernott, J.P., Shrager, J., Silflow, C. and Stern, D.
 TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
 Unicellular System for Analyzing Gene Function and Regulation in
 Vascular Plants. Project: 1031
 JOURNAL Unpublished (2001)
 COMMENT Contact: Charles Hauser
 DCMB Box 91000
 Duke University
 Durham, NC 27708-1000
 Tel: 919 613 8159
 Fax: 919 613 8177
 Email: chauser@duke.edu.

FEATURES
 source
 1..666
 /organism="Chlamydomonas reinhardtii"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
 /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
 XhoI; Stress condition II library, constructed by John
 Davies and Jeffrey McDermott, combines cDNAs from CC-1690
 cells grown to mid-log phase in TAP (NH4+ - containing)
 and shifted to TAP - NO3- (24hrs); H2 production
 conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
 Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
 sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
 PolyA mRNA was purified from each sample, pooled and cDNA
 synthesized. The cDNA was directionally cloned into lambda
 Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
 sites. pBluescript II SK- plasmids were excised from the
 lambda Zap clones by superinfection with ExAssist
 (Stratagene) phage. The library was normalized using
 method 4 described in Bonaldo et al., (1996) Genome
 Research 6: 791-806."
 Research 6: 791-806."
 BASE COUNT 121 a 244 c 224 g 77 t
 ORIGIN

Query Match 23.3%; Score 456; DB 13; Length 666;
 Best Local Similarity 100.0%; Pred. No. 1.9e-68;
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 TGGGAGGCGCTGTGGAGAGGTGGTGTACGGCAAGGGCGGCTGGCCACCGCAAGAAG 1557
 |||||
 Db 1 TGGGAGGCGCTGTGGAGAGGTGGTGTACGGCAAGGGCGGCTGGCCACCGCAAGAAG 60
 |||||

QY 1558 GAGGAGATCAAGGTGCGCGCTTGGCGAGAGATCCCCGGGACCTGCCCGCGGTCTCTAC 1617
 |||||
 Db 61 GAGGAGATCAAGGTGCGCGCTTGGCGAGAGATCCCCGGGACCTGCCCGCGGTCTCTAC 120
 |||||
 QY 1618 GCCCCCAACACCTTGAAGCCCGTGTCCGCTCCGTGAGGGGACACGGCGCGCGCC 1677
 |||||
 Db 121 GCCCCCAACACCTTGAAGCCCGTGTCCGCTCCGTGAGGGGACACGGCGCGCGCC 180
 |||||
 QY 1678 AAGTCTGGGACACCGCCCGCCGCGCATGGCGCGTGGCGCGGACACCCCTCTCGGGCCCC 1737
 |||||
 Db 181 AAGTCTGGGACACCGCCCGCCGCGCATGGCGCGTGGCGCGGACACCCCTCTCGGGCCCC 240
 |||||
 QY 1738 TCGCCCGCCCGCGCCACCCCAAGGTGACCACTACAAAGCCCGCGCTCGCGCGCACCGCC 1797
 |||||
 Db 241 TCGCCCGCCCGCGCCACCCCAAGGTGACCACTACAAAGCCCGCGCTCGCGCGCACCGCC 300
 |||||
 QY 1798 AAGCCCAAGACCGCTGCGCTCAAGCTGCGCGTGGAGCCCTCCACACTGACCTCGGAG 1857
 |||||
 Db 301 AAGCCCAAGACCGCTGCGCTCAAGCTGCGCGTGGAGCCCTCCACACTGACCTCGGAG 360
 |||||
 QY 1858 AAGCGCGCTGCTCCAAACGGCAACGGCAAGGTGCTTCGGCTCCAAAGACTTCGGCTGCC 1917
 |||||
 Db 361 AAGCGCGCTGCTCCAAACGGCAACGGCAAGGTGCTTCGGCTCCAAAGACTTCGGCTGCC 420
 |||||
 QY 1918 AAGCCCTGTGCTCCGCGCGCCACCCGCAAGTCCGCC 1953
 |||||
 Db 421 AAGCCCTGTGCTCCGCGCGCCACCCGCAAGTCCGCC 456
 |||||

RESULT 6
 LOCUS AY109531 2147 bp mRNA linear HTC 25-MAY-2002
 DEFINITION Zea mays CL1198_1 mRNA sequence.
 ACCESSION AY109531
 VERSION AY109531.1 GI:21213285
 KEYWORDS HTC.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 2147)
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 JOURNAL Unpublished (2002)
 REFERENCE 2 (bases 1 to 2147)
 AUTHORS Coe, E.C.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 FEATURES
 Location/Qualifiers
 1..2147
 /organism="Zea mays"
 /db_xref="MaizeDB:630100"
 /db_xref="taxon:4577"
 /clone="CL1198_1"
 /clone_lib="Maize Mapping Project/DuPont Consensus
 Library"
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed DuPont contigs; this resource was
 assembled by DuPont as part of a collaboration with the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

BASE COUNT 400 a 582 c 604 g 365 t 196 others
 ORIGIN
 Query Match 23.3%; Score 454.6; DB 11; Length 2147;
 Best Local Similarity 58.6%; Pred. No. 3.8e-68;
 Matches 910; Conservative 0; Mismatches 547; Indels 96; Gaps 6;

Matches 456; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 365 AGGCTGCCCGCTGCTGCCCTTCGGCCGGGAGGAGTCTCTTCCTGCGCCAAAGACT 424
Db 1 AGGCTGCCCGCTGCTGCCCTTCGGCCGGGAGGAGTCTCTTCCTGCGCCAAAGACT 60
QY 425 GGCACCTCCGCCCTGGTGGCCCTGCTGCTGAAGGACGAGTACCAAGCCCAAGGGCCAGTTCA 484
Db 61 GGCACCTCCGCCCTGGTGGCCCTGCTGCTGAAGGACGAGTACCAAGCCCAAGGGCCAGTTCA 120
QY 485 CCAAGGCCAAGTCTGGTGGCTATC-CACACATCGCCCTTCAGAGGCCGATGTGGAG 543
Db 121 CCAAGGCCAAGTCTGGTGGCTATCGCACAAATCGCCTTCAGAGGCCGATGTGGAG 180
QY 544 GAGGCTTCAAGGACACGAGTGGCCAGGCGGCTTTGACAAGCTGGCTTCGAGAC 603
Db 181 GAGGCTTCAAGGACATGAGTGGCCAGGCGGCTTTGACAAGCTGGCTTCGAGAC 240
QY 604 GGCTATGCCAAGTTTACACTGAGGCCACCCCATGAGGAGGACGAGAGCCCGCGTG 663
Db 241 GGCTATGCCAAGTTTACACTGAGGCCACCCCATGAGGAGGACGAGAGCCCGCGTG 300
QY 664 ACGGGAAGACCTACGAAGATCACTGGCTGAAGGGTGGCATTTATCGCCGCGACAAG 723
Db 301 ACGGGAAGACCTACGAAGATCACTGGCTGAAGGGTGGCATTTATCGCCGCGACAAG 360
QY 724 CTGGTACTGTGTGCGCCAACTACGCGACGAGATCGCTGCGATCGCGCGCGGTGTG 783
Db 361 CTGGTACTGTGTGCGCCAACTACGCGACGAGATCGCTGCGATCGCGCGCGGTGTG 420
QY 784 GAGCTGGACACCTGATCGCGCCCAAGGGCAATTGAGGG 821
Db 421 GAGCTGGACACCTGATCGCGCCCAAGGGCAATTGAGGG 458

RESULT 8
AV629117 436 bp mRNA linear EST 15-DEC-2000
LOCUS AV629117 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas
DEFINITION reinhardtii cDNA clone LCL052d05_r 5', mRNA sequence.
ACCESSION AV629117
VERSION AV629117.1 GI:10791751
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 436)
AUTHORS Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y., and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
source
1. .436
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="LCL052d05_r"
/note="Vector: pBluescriptII SK; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from 5% to 0.04%"
BASE COUNT 66 a 145 c 138 g 87 t
ORIGIN

Query Match 20.5%; Score 400.8; DB 10; Length 436;
Best Local Similarity 99.5%; Pred. No. 5e-59;
Matches 402; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGCCTGGACATCGTGTGTTGCTGCTGAGGTGCGCCCTTGGTCCCAAGAGCGGCGCTG 60
Db 33 GGCCTGGACATCGTGTGTTGCTGCTGAGGTGCGCCCTTGGTCCCAAGAGCGGCGCTG 92
QY 61 GGCATGTGACTGCTGGCTGCTGCTATTGAGTGTCAAGCGCGCCACCGCTCATGACC 120
Db 93 GGCATGTGACTGCTGGCTGCTGCTATTGAGTGTCAAGCGCGCCACCGCTCATGACC 152
QY 121 ATTGCCCTCGCTGCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 153 ATTGCCCTCGCTGCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 212
QY 181 ATGGGCGAGNAGTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 213 ATGGGCGAGNAGTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272
QY 241 GACCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 273 GACCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 332
QY 301 CGCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 333 CGCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 392
QY 361 ATTGAGGCTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
Db 393 ATTGAGGCTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436

RESULT 9
AV394077 511 bp mRNA linear EST 23-APR-2002
LOCUS AV394077 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
DEFINITION cDNA clone CL18c08_r 5', mRNA sequence.
ACCESSION AV394077
VERSION AV394077.1 GI:6548293
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 511)
AUTHORS Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H., and Tabata, S.
TITLE A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)
MEDLINE 20152988
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
source
1. .511
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="CL18c08_r"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK; Site 1: EcoRI; Site 2: XhoI"
BASE COUNT 80 a 170 c 159 g 101 t 1 others
ORIGIN
Query Match 20.3%; Score 395.6; DB 10; Length 511;
Best Local Similarity 98.8%; Pred. No. 3.9e-58;

Matches 398; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 GCGCTGGACATCGTCATGCTGCTGCTGAGTTCGCGCCCTTGGTCCAGACGGGGGCGCTG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
109 GCGCTGGACATCGTCATGCTGCTGCTGAGTTCGCGCCCTTGGTCCAGACGGGGGCGCTG 168
QY 61 GCGGATGTGACTGTGTGCGCTGCCTATTGAGCTGTGTCAGCGCGGCCACCGGCTCATGACC 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
169 GCGGATGTGACTGTGTGCGCTGCCTATTGAGCTGTGTCAGCGCGGCCACCGGCTCATGACC 228
QY 121 ATTGCCCTCGCTACGACACAGTACGCTGACCGCTGGGACACCTCGGTGGACATC 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
229 ATTGCCCTCGCTACGACACAGTACGCTGACCGCTGGGACACCTCGGTGGACATC 288
QY 181 ATGGCGGAGAGGTCGCTACTTCCATCCATCAAGAGGCGCTGACCGGCTGTGGAT 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
289 ATGGCGGAGAGGTCGCTACTTCCATCCATCAAGAGGCGCTGACCGGCTGTGGAT 348
QY 241 GACACCCCTGGTTCCTGGCCAGGCTGTGGGCAAGACCGGCTCCAGCTGTACGGCCCC 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
349 GACACCCCTGGTTCCTGGCCAGGCTGTGGGCAAGACCGGCTCCAGCTGTACGGCCCC 408
QY 301 CGTCCGGCGCTGACTACCTGGACCAACCAAGCGCTTCGCCCTGTCTGCAAGGCGCT 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
409 CGTCCGGCGCTGACTACCTGGACCAACCAAGCGCTTCGCCCTGTCTGCAAGGCGCT 468
QY 361 ATTGAGGCTGCCCGCGCTGCTGCCCTTCGGCCCGCGGAGGACT 403
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
469 ATAGAGGCTNGCGGCTGCTGCCCTTCGGCCCGCGGAGGACT 511

```

```

RESULT 10
AV631115
LOCUS
DEFINITION AV631115 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas
reinhardtii cDNA clone LCL089a12_r 5', mRNA sequence.
ACCESSION AV631115
VERSION AV631115.1 GI:10793749
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
AUTHORS Asamizu,E., Mura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..393
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="LCL089a12_r"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
64 a 145 c 137 g 47 t

```

```

FEATURES
source
Query Match 20.0%; Score 391.4; DB 10; Length 393;
Best Local Similarity 99.7%; Pred. No. 2e-57;
Matches 392; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
BASE COUNT
ORIGIN
64 a 145 c 137 g 47 t

```

```

QY 1327 ACCGCTTCCATCATGGCGCCCTGAACCCGACAAAGCTGAGCTGACGCGACGCC 1386
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 ACCGCTTCCATCATGGCGCCCTGAACCCGACAAAGCTGAGCTGAGCTGACGCGACGCC 60
QY 1387 CTGGCCGCCACCGTGGCGCGCTGCCAGCGAGTGTTCGGGGGCGCGCTACCCCGAGATG 1446
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 CTGGCCGCCACCGTGGCGCGCTGCCAGCGAGTGTTCGGGGGCGCGCTACCCCGAGATG 120
QY 1447 GTGGCCAACCTGCATCAGCCAGGACCTGTCTGGTTCACAGCCCGCCCGAAGTGGAGGCG 1506
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 GTGGCCAACCTGCATCAGCCAGGACCTGTCTGGTTCACAGCCCGCCCGAAGTGGAGGCG 180
QY 1507 CTGCTGAGGAGGTGTGTACGGCAAGGCGCGTGGCCACCGCAAGAGGAGGATC 1566
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 CTGCTGAGGAGGTGTGTACGGCAAGGCGCGTGGCCACCGCAAGAGGAGGATC 240
QY 1567 AAGTGCCCGTTCGGGAGAGATCCCGGCGACCTGCGCGCGTGTCTACGCCCGCCCAAC 1626
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 AAGTGCCCGTTCGGGAGAGATCCCGGCGACCTGCGCGCGTGTCTACGCCCGCCCAAC 300
QY 1627 ACCCTGAAGCCCGTGTCCGCTCGTGGAGGCAACGCGCGCGCGCGCGCGCGCGCG 1686
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 ACCCTGAAGCCCGTGTCCGCTCGTGGAGGCAACGCGCGCGCGCGCGCGCGCGCGCG 360
QY 1687 ACCACGCGCGCGCGCATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1719
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 ACCACGCGCGCGCGCATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 393

```

```

RESULT 11
AW757933
LOCUS
DEFINITION 874004E12.y1 C. reinhardtii CC-1690, Lambda zap II Chlamydomonas
reinhardtii cDNA, mRNA sequence.
ACCESSION AW757933
VERSION AW757933.1 GI:7687285
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers
1..475
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Lambda zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)

```


cells grown to mid-log phase in TAP (NH₄⁺ - containing) and shifted to TAP - NO₃⁻ (24hrs); H₂ production conditions (0, 12hr, 24hr) see Melis et al., (2000) plant Phys. 122: 127-135; TAP + H₂O₂ (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

BASE COUNT 59 a 169 c 102 g 37 t
ORIGIN

Query Match 18.1%; Score 352.6; DB 13; Length 367;
Best Local Similarity 97.9%; Pred. No. 8 5e-51;
Matches 370; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCTGACATCGTGATGGTGTCTGAGTTCGCGCCCTTGGTCCAGAGCGGCGCCTGG 61
|||||
Db 98 CGCTGGACATCGTATGGTGTCTGAGTTCGCGCCCTTGGTCCAGAGCGGCGCCTGG 157
|||||

QY 62 GCGATGTGACTGCTGGCCTGCCTATTGACTGTGTCGCAAGCGCGCCACCGCGTCATGACCA 121
|||||
Db 158 GCGATGTGACTGCTGGCCTGCCTATTGACTGTGTCGCAAGCGCGCCACCGCGTCATGACCA 217
|||||

QY 122 TTGCCCCCTCGCTACGACCAAGTACGCTGAGCGCTGGGACACCTCGTGCTGGGACATCA 181
|||||
Db 218 TTGCCCCCTCGCTACGACCAAGTACGCTGAGCGCTGGGACACCTCGTGCTGGGACATCA 277
|||||

QY 182 TGGGCGAGAGGTTCGCTACTTCCACTCCATCAAGAAGGCGGTGACCGCGTGTGGATTG 241
|||||
Db 278 TGGGCGAGAGGTTCGCTACTTCCACTCCATCAAGAAGGCGGTGACCGCGTGTGGATTG 337
|||||

QY 242 ACCACCCCTGGTTCCTGGCCAAAGTCTGGGCAAGACCGCGCTCCAAAGCTGTAGCGCCCC 301
|||||
Db 338 ACCACCCCTGGTTCCTGGCCAAAGTCTGGGCAAGACCGCGCTCCAAAGCTGTAGCGCCCC 397
|||||

QY 302 GCTCGGGCGCTGACTACCTGGGCAACCAAGCGCTTCGCCCTGTTCGCAAGCGCGCTA 361
|||||
Db 398 GCTCGGGCGCTGACTACCTGGGCAACCAAGCGCTTCGCCCTGTTCGCAAGCGCGCTA 457
|||||

QY 362 TTGAGCTGCGCGCGTGC 379
|||||
Db 458 TTGAGCTGCGCGCGTGC 475
|||||

RESULT 12
BI727902
LOCUS 1031095E03.y1 C. reinhardtii CC-1690, Stress II (normalized),
DEFINITION Lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
BI727902
BI727902
VERSION 1
KEYWORDS EST.
SOURCE GI:15703597
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
AUTHORS Analyses of the Chlamydomonas reinhardtii Genome: A Model,
TITLE Unicellular System for Analyzing Gene Function and Regulation in
JOURNAL Vascular Plants. Project: 1031
COMMENT Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1. .367
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized)
), Lambda zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690

BASE COUNT 59 a 169 c 102 g 37 t
ORIGIN

Query Match 18.1%; Score 352.6; DB 13; Length 367;
Best Local Similarity 98.9%; Pred. No. 8 5e-51;
Matches 355; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1582 GAGAAGATCCCGCGGACCTGCGCGCGTGTCTACGCCGCCAACACCTTGAGCGCGTG 1641
|||||
Db 9 GAGAAGATCCCGCGGACCTGCGCGCGTGTCTACGCCGCCAACACCTTGAGCGCGTG 68
|||||

QY 1642 TCGGCTTCGTGAGGCAACGCGCGCGCGCCGCGCAAGGTGCGCACCCGCCCGCC 1701
|||||
Db 69 TCGGCTTCGTGAGGCAACGCGCGCGCGCCGCGCAAGGTGCGCACCCGCCCGCC 128
|||||

QY 1702 ATGGCGCGTGGCGCGGACCGCGCGCTCGGGCGCGCTCGCGCGCGCGCGCGCGCGCG 1761
|||||
Db 129 ATGGCGCGTGGCGCGGACCGCGCGCTCGGGCGCGCTCGCGCGCGCGCGCGCGCGCG 188
|||||

QY 1762 GTGACCACTTACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1821
|||||
Db 189 GTGACCACTTACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 248
|||||

QY 1822 CTGGCGGTGAGGCTCCACCACTCGACCTCGGAGAACGCGCGCTGCTCCACGCGCAAC 1881
|||||
Db 249 CTGGCGGTGAGGCTCCACCACTCGACCTCGGAGAACGCGCGCTGCTCCACGCGCAAC 308
|||||

QY 1882 GGCACCGTTCCTGGCGCTCCAGACCTCGGCTGCCAAGCGCGCGCGCGCGCGCGCG 1940
|||||
Db 309 GGTACCGTTCCTGGCGCTCCAGACCTCGGCTGCCAAGCGCGCGCGCGCGCGCGCG 367
|||||

RESULT 13
BF863935
LOCUS 963047G01.y1 C. reinhardtii CC-1690, Stress condition I, normalized
DEFINITION Lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
BF863935
BF863935
VERSION 1
KEYWORDS EST.
SOURCE GI:12254079
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
AUTHORS Analyses of the Chlamydomonas reinhardtii Genome: A Model,
TITLE Unicellular System for Analyzing Gene Function and Regulation in
JOURNAL Vascular Plants. Project: phase 3
COMMENT Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1. .799

/organism="Chlamydomonas reinhardtii"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_lib="C. reinhardtii CC-1690, Stress condition I,
 normalized, Lambda Zap II"
 /note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2:
 XhoI; This library, constructed by John Davies and Jeffrey
 McDermott, combines cDNAs from CC-1690 cells grown to
 mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
 1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). POLYA mRNA was
 purified from each sample, pooled and cDNA synthesized.
 The cDNA was directionally cloned into lambda Zap II
 (Stratagene) in the EcoRI (5') and XhoI (3') sites.
 pBluescript II SK- plasmids were excised from the lambda
 Zap clones by superinfection with ExAssist (Stratagene)
 phage. The library was normalized using method 4 described
 in Bonaldo et al (1996) Genome Research 6: 791-806."
 BASE COUNT 141 a 256 c 208 g 193 t 1 others
 ORIGIN

Query Match 18.0%; Score 351.2; DB 12; Length 799;
 Best Local Similarity 98.9%; Pred. No. 1.6e-50;
 Matches 364; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1155 GGTCAAGTTCTCGCGCCCTGGCGGCACATGCTCACGCGCGCGCGACTTCATGCTGGT 1214
 |||||||
 Db 124 GGTCAAGTTCTCGCGCCCTGGCGGCACATGCTCACGCGCGCGCGACTTCATGCTGGT 183
 |||||||
 QY 1215 GCCCTCGGTTGAGCCCTCGCGCTGATCCAGCTGCACGCCATGACCTACGTTACCGT 1274
 |||||||
 Db 184 GCCCTCGGTTGAGCCCTCGCGCTGATCCAGCTGCACGCCATGACCTACGTTACCGT 243
 |||||||
 QY 1275 GCCCTGTTAGCTCGACCGCGGCGCTGTCGACACCGTCAAGGAGGCGGCTACCGGCTT 1334
 |||||||
 Db 244 GCCCTGTTAGCTCGACCGCGGCGCTGTCGACACCGTCAAGGAGGCGGCTACCGGCTT 303
 |||||||
 QY 1335 CCATATGGCGCCCTGAACCCCGACAGCTGGAGAGGCTGACGCCAGCTGTTGGCCAA 1454
 |||||||
 Db 304 CCATATGGCGCCCTGAACCCCGACAGCTGGAGAGGCTGACGCCAGCTGTTGGCCAA 423
 |||||||
 QY 1455 CTGATCAGCCAGGACCTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1513
 |||||||
 Db 424 CTGATCAGCCAGGACCTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 483
 |||||||
 QY 1514 AGGAGGTG 1521
 |||||||
 Db 484 AGGAGGTG 491

RESULT 14
 AV644765
 LOCUS
 DEFINITION AV644765 418 bp mRNA linear EST 15-DEC-2000
 CDNA clone HCL093d12_r 5', mRNA sequence.
 AV644765
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Chlamydomonas reinhardtii.
 Chlamydomonas reinhardtii.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadaceae; Chlamydomonas.
 1 (bases 1 to 418)
 Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohshima, K.,
 Nakamura, Y. and Tabata, S.
 Generation of expressed sequence tags from low-CO2 and high-CO2
 adapted cells of Chlamydomonas reinhardtii
 DNA Res. 7 (5), 305-307 (2000)
 20539644

COMMENT
 Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
 source
 1. 418
 /organism="Chlamydomonas reinhardtii"
 /strain="C9"
 /db_xref="taxon:3055"
 /clone="HCL093d12_r"
 /clone_lib="Chlamydomonas reinhardtii 5% CO2"
 /note="Vector: pBluescriptII SK-; Site.1: EcoRI; Site.2:
 XhoI; The cDNA library was constructed from cells cultured
 in a medium with bubbling air containing 5% carbon
 dioxide"
 BASE COUNT 65 a 139 c 130 g 84 t
 ORIGIN

Query Match 17.3%; Score 337.8; DB 10; Length 418;
 Best Local Similarity 99.4%; Pred. No. 2.9e-48;
 Matches 339; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGCTGACATCGTATGGTTCGCTGAGGTGCGCCCTTGGTCCAAAGACGGGCGCTG 60
 |||||||
 Db 78 GCGCTGGACATCGTATGGTTCGCTGAGGTGCGCCCTTGGTCCAAAGACGGGCGCTG 137
 |||||||
 QY 61 GCGATGTGACTGTGGCTGCCTATTGAGCTGCTCAAGCGGCGCCACCGGCTCATGACC 120
 |||||||
 Db 138 GCGATGTGACTGTGGCTGCCTATTGAGCTGCTCAAGCGGCGCCACCGGCTCATGACC 197
 |||||||
 QY 121 ATTGCCCTCGCTACGACACAGTACGCTGACGCTGGGACACCTCGTGTGCTGGACATC 180
 |||||||
 Db 198 ATTGCCCTCGCTACGACACAGTACGCTGACGCTGGGACACCTCGTGTGCTGGACATC 257
 |||||||
 QY 181 ATGGCGAGAGGTCGCTACTTCCACATCAAGAGGCGGTCACCGGCTGTGGATT 240
 |||||||
 Db 258 ATGGCGAGAGGTCGCTACTTCCACATCAAGAGGCGGTCACCGGCTGTGGATT 317
 |||||||
 QY 241 GACCACCCCTGTTCTTGGCCAAAGTCTGGGCGAGACCGGCTCCAGCTGTAGGCCCC 300
 |||||||
 Db 318 GACCACCCCTGTTCTTGGCCAAAGTCTGGGCGAGACCGGCTCCAGCTGTAGGCCCC 377
 |||||||
 QY 301 CGTCCGCGCTGACTACTACCTGGACCAACACAAAGCGCTTCGC 341
 |||||||
 Db 378 CGTCCGCGCTGACTACTACCTGGACCAACACAAAGCGCTTCGC 418

RESULT 15
 AV643281
 LOCUS
 DEFINITION AV643281 506 bp mRNA linear EST 15-DEC-2000
 CDNA clone HCL066h09_r 5', mRNA sequence.
 AV643281
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Chlamydomonas reinhardtii.
 Chlamydomonas reinhardtii.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadaceae; Chlamydomonas.
 1 (bases 1 to 506)
 Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohshima, K.,
 Nakamura, Y. and Tabata, S.
 Generation of expressed sequence tags from low-CO2 and high-CO2
 adapted cells of Chlamydomonas reinhardtii
 DNA Res. 7 (5), 305-307 (2000)
 20539644
 Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

```
source
1. .506
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="HCL066H09_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
BASE COUNT      77 a   170 c   160 g   99 t
ORIGIN
Query Match      15.1%; Score 295.8; DB 10; Length 506;
Best Local Similarity 99.3%; Pred. No. 4.5e-41;
Matches 297; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCGCTGGACATCGTGAATGTTGCTGTGAGTGGCGCCCTTGGTCCAAAGACGGCGGCTCG 60
Db 208 GCGCTGGACATCGTGAATGTTGCTGTGAGTGGCGCCCTTGGTCCAAAGACGGCGGCTCG 267
QY 61 GCGCATGTGACTGTGGCTGCTATATGAGTGGTCAAGGGCGGCCACCGCGTCATGACC 120
Db 268 GCGCATGTGACTGTGGCTGCTATATGAGTGGTCAAGGGCGGCCACCGCGTCATGACC 327
QY 121 ATTGCCCTCGCTACGACCACTACGCTGACCGCTGGGACACACCTCGGTGGTGGGACATC 180
Db 328 ATTGCCCTCGCTACGACCACTACGCTGACCGCTGGGACACACCTCGGTGGTGGGACATC 387
QY 181 ATGGGGGAGAAGTTCGGCTACTTCCACTCCATCAAGAAGGGCGTGCACCGCGTGTGGATT 240
Db 388 ATGGGGGAGAAGTTCGGCTACTTCCACTCCATCAAGAAGGGCGTGCACCGCGTGTGGATT 447
QY 241 GACCAACCTGTGTTCTGCGCAAGGTCTGGGGCAAGACCGGCTCCAAAGCTGTACGGCCC 299
Db 448 GACCAACCTGTGTTCTGCGCAAGGTCTGGGGCAAGACCGGCTCCAAAGCTGTACGGCCC 506
```

Search completed: June 3, 2003, 15:27:21
Job time : 1915.46 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 09:49:44 ; Search time 46.9794 Seconds
(without alignments)
12748.991 Million cell updates/sec

Title: US-09-980-771A-4

Perfect score: 1953

Sequence: 1 gcgcggacatcgtgatgt.....ccgccaccgcgaagtcgcgc 1953

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2.6/prodata/1/ina/5A_COMB.seq.*
2: /cgn2.6/prodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/prodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2.6/prodata/1/ina/PCrus_COMB.seq.*
6: /cgn2.6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475.8	24.4	2267	4	US-08-679-645-25
2	447.4	22.9	2542	3	US-08-941-445A-6
3	276.2	14.1	2067	4	US-09-388-743-21
4	266.6	13.7	2274	4	US-09-388-743-17
5	259.6	13.3	2176	4	US-09-388-743-13
6	255.4	13.1	2202	4	US-09-388-743-1
7	218.2	11.2	2825	4	US-09-196-390-5
8	216.8	11.1	2097	3	US-08-941-445A-10
9	210.8	10.8	2380	1	US-08-572-951-3
10	207	10.6	2248	4	US-09-345-214-20
11	206.6	10.6	1798	4	US-09-345-214-16
12	206.6	10.6	2019	4	US-09-345-214-15
13	161	8.2	2007	3	US-08-941-445A-8
14	161	8.2	2085	1	US-08-572-951-2
15	118.2	6.1	2239	4	US-09-196-390-1
16	109.6	5.6	2348	4	US-09-388-743-5
17	108	5.5	1758	3	US-08-836-567-3
18	106.8	5.5	2277	1	US-08-676-967-5
19	106.8	5.5	2277	1	US-08-676-974-5
20	106.8	5.5	2277	2	US-09-098-487-5
21	106.8	5.5	2418	4	US-09-388-743-25
22	106.6	5.5	2360	3	US-08-836-567-9
23	102.6	5.3	1528	4	US-09-345-214-6
24	102.6	5.3	1620	3	US-08-941-445A-20
25	102.6	5.3	1752	3	US-08-941-445A-12
26	102.6	5.3	2008	4	US-09-345-214-12
27	102.6	5.3	2491	4	US-09-345-214-5

28 102 5.2 2712 3 US-09-025-691-4
29 101 5.2 2383 4 US-09-192-909-1
c 30 99 5.1 4403765 4 US-09-103-840A-2
31 97.8 5.0 2990 1 US-08-572-951-1
32 97.4 5.0 4800 3 US-08-941-445A-4
33 91.2 4.7 4403765 4 US-09-103-840A-2
34 89.2 4.6 2793 3 US-08-836-567-7
35 88.4 4.5 6027 2 US-08-968-542C-1
36 86.8 4.4 2809 3 US-05-000-016-1
37 86.8 4.4 2809 4 US-03-514-340-1
38 86.4 4.4 44377 2 US-08-804-227C-7
39 86.4 4.4 44377 2 US-08-804-198-1
c 40 84.6 4.3 985 4 US-09-056-556-182
c 41 84.6 4.3 985 4 US-09-072-596-177
42 84.6 4.3 1620 2 US-08-461-775-10
43 84.6 4.3 1620 3 US-09-031-606-10
44 84.4 4.3 1926 3 US-08-836-567-5
45 82.6 4.2 1464 1 US-07-735-065-1

ALIGNMENTS

RESULT 1
US-08-679-645-25
; Sequence 25, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 25:

Sequence 4, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 182, App
Sequence 177, App
Sequence 10, Appl
Sequence 10, Appl
Sequence 5, Appli
Sequence 1, Appli

SEQUENCE CHARACTERISTICS:
; LENGTH: 2267 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-679-645-25

Query Match 24.4%; Score 475.8; DB 4; Length 2267;
Best Local Similarity 59.9%; Pred. No. 2.3e-74;
Matches 979; Conservative 0; Mismatches 557; Indels 99; Gaps 7;
QY 5 TGGACATCGTGATGTTGCTGAGTCTGCGCCCTTGGTCCAAAGACGGGCGCTGGGG 64
Db 418 TGAACGTCGCTTCGTGCGCGCGAGATGGCGCGTGGAGCAAGACCGCGCGCTCGGG 477
QY 65 AATGACTGGTGGCTGCTATGAGCTGGTCAAGCGCGGCCACCGCTCATCAACATTG 124
Db 478 AGTCTCTCGCGCGCTTGGCGCGCGCATGGCGCGAATGGCGACCGCTGATGCTGT 537
QY 125 CCGCTCGCTACGACCACTAGCTGACGCTGGACACCTCGGTGGTGGGACAT----- 179
Db 538 CTCCTCGCTACGACCACTAGCTGACGCTGGACACCGCTGGGACCGCTGCTGGAGTCAAGA 597
QY 180 -----CATGGCGAGAGGTCGGTACTTCCATCCATCAAGAGGGGGTGCACGGG 232
Db 598 TGGGAGACAGGTACGAGAGGTCAGGTTCTTCCACTGCTACAAAGCGCGGAGTGCACGGG 657
QY 233 TGTGGATTACCAACCTCTGCTTCCGCAAGCTTGGGCAAGCGCGGTCCCAAGCTGT 292
Db 658 TGTGCTGTACCAACCTCTGCTTGGAGAGGTTTGGGAAAGACCGGAGGAGAAGATCT 717
QY 293 ACGGCGCGCGCTCGGCGGTGACTACTGGACAACCAACAGCGCTTGGCGCTTCTTGCA 352
Db 718 ACGGCGCTGACGCTGGAACGACTACAGGAGCAACAGCTGCGGTTTCAAGCTGCTATGOC 777
QY 353 AGCGCGCTATTAGGCTGCGCGGTGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 390
Db 778 AGGAGCACTTGAAGTCCAAAGATCCTGAGCCTCAACAAACCCATATCTTCCGGAC 837
QY 391 --CCGCGGAGGAGTGGTCTTGGTGGCAACGACTGGCACTCGCGCTTGGTGGCGTCC 448
Db 838 CATACGGGAGGAGCTGCTGCTGCTGCAACGACTGGCACCGGCGCTTCTCGTGTCT 897
QY 449 TGTGAAGGAGGAGTACCAAGCGCAAGGCGAGTTCACCAAGGCCAAGTCTGGTGTGCTA 508
Db 898 ACCTCAAGAGCAACTACCACTCCACGGCATCTACAGGGACGCAAGACCGCTTCTGCA 957
QY 509 TCACACATCGCTTCCAGGCGCGATGTGGAGGAGGCTTTCAGGACACGAGCTGC 568
Db 958 TCACACATCTCTCTACGAGGCGGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1017
QY 569 CCGAGCGCGCTTTCAGCAAGCTGCGCTTCTCGGACGCTATGCCAAGGTTTACACTGAGG 628
Db 1018 CGGAGATTCAGTGTCTCTGATTCATGACGCGCTACGAGAAG----- 1064
QY 629 CCACCCCATGAGGAGGAGGAGAGAGCGCGCGCTGACGGGAAGACCTACAAGAGATCA 688
Db 1065 -----CCGCTGGAAG-----GCCGGAAGATCA 1086
QY 689 ACTGGCTGAAGGTTGGGATTCGCGCGCGAGCTGTTGACTGTGTCGCCCAACTACG 748
Db 1087 ACTGGATGAAGGCGGATCTCGAGCGCGAGAGGCTCTACCGCTGAGCGCTTACTACG 1146
QY 749 CGACCGAGATGCTTGGGATGCCCGCGGCTGAGCTGGACACCGCTCATCGCGCCA 808
Db 1147 CCGAGGAGCTCATCTCCGCGATCGCCAGGGCTCGGAGCTCGACAACATCATGGCGCTCA 1206
QY 809 AGGCAATTGAGGCGATTGTGAACGGATGACATTTAGGAGTGAACCCCAAGACCGACA 868
Db 1207 CCGGCATCACCGGATCGTCAACGGCATTGGAGCTTCAGGCTGGGACCCCAAGAGGACA 1266
QY 869 AGTTCCTGTGCGCTTACCAACAGAACAGCTTACGCGGCAAGCGCCGCCCAAGG 928

Db 1267 AGTACATCGCGTGAAGTAGACAGTGTGACGCGCGTGGAGGCCAAGGCGCTCAACAAGG 1326
QY 929 AGGCCCTGACGCGGAGCTGGGCTGCTGTGTGACCCCAACCGCCCGCTTTCGCGCTCA 988
Db 1327 AGCGCTGACGCGGAGGTCGGCTCCCGGTGACCGGAACATCCCGCTGCTGGCGCTTCA 1386
QY 989 TCGGCGCGCTGGAGGACGAGAGGTTGGACATCATCTTGGCGCGCGCTTCCCAAGATCC 1048
Db 1387 TCGGCGGCTGGAAGACGAGAGGACCGCGCATGTCGCGCGCGCATCCCGAGCTCA 1446
QY 1049 TGGCCACCCCAAG---GTGCAGATCGCATCTCTGGTACCGCAAGCGCGCTACGAGA 1105
Db 1447 TGGAGATGTTGGAGGAGCTGCAGATCTTCTGTGGCACGGGCAAGAAAGTTGAGC 1506
QY 1106 AGCTGTGAACGCGCATCGGACCAAGTACAAAGGCGCGCGCAAGGGCGTGGTCAAGTTCT 1165
Db 1507 GCATGCTCATGAGCGCGGAGGAGAGTTCCAGGCAAGTGTGCGCGCTGTTCAAGTTCA 1566
QY 1166 CGCGCGCGCTGGCGACATGCTCACCGCGCGCGCGCGCTTTCATGCTGCTGCTCGCGCT 1225
Db 1567 ACGCGCGCTTGGCGCACCATCATGCGCGCGCGCGCGCTGCTGCGCGCTCACGACGCGCT 1626
QY 1226 TCGAGCGCTCGCGCTGATCCAGCTGACGCGCATGTGACTACGCTACGCTGCGCGCTGGTAG 1285
Db 1627 TCGAGCGCTCGCGCTCATCCAGCTGAGGAGTGCATACGAGAACCGCTTGGCGCTGCG 1686
QY 1286 CTTCCACCGCGCGCTTGGTGCACACCGCTCAAGGAGGCGCTCACCGGCTTCCACATGCGG 1345
Db 1687 CGTCCACCGCTGCGCTGCGACACCATCATCGAAGGCAAGACGCGGTTCCACATGGGCG 1746
QY 1346 CCGTGA-----ACCCGCAAGCTGACGAGGCTGACGCGCGAGCGCTTGGCGCGCACCG 1399
Db 1747 GCCTACGCTGCACTGCAAGCTGCTGGAGCGCGCGAGCTCAAGAAAGTGGCCACCACT 1806
QY 1400 TGGCGCTGCGCAGGAGTGTTCGCGCGCGCGCTTACCCCGAGATGTTGGGCCAACTGCA 1459
Db 1807 TGCAGCGCGCATCAAGTGTGCGCACCGCGCGCTGACGAGGAGATGTTGAGGAACTGCA 1866
QY 1460 TCAGCCAGGAGCTGCTGCTGTCAGCGCGCGCGCGCGCGAGTGGAGGCGCTTCTGGAGGAG 1519
Db 1867 TGAATCCAGGATCTCTCTGGAAGGCGCTTCCAAAGAACTGGGAGAACTGCTGCTGAGCC 1926
QY 1520 TGGTGTACGCAAGGCGCGCTGCGCACCGCGCAAGAGGAGGAGATCAAGGTGCGCGTTG 1579
Db 1927 TCGGGGTGCGC---GGCGCGAGCGAGGCTGGAAGCGGAGATCGCGCGCTCGCCA 1983
QY 1580 CCGAGAAGATCCCGC 1594
Db 1984 AGGAGAAGTGGCGC 1998

RESULT 2
US-08-941-445A-6
; Sequence 6, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

: APPLICATION NUMBER: US/08/941,445A
: FILING DATE: 30-SEP-1997
: CLASSIFICATION: 800
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 60/026,855
: FILING DATE: 30-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Winner, Ellen P
: REGISTRATION NUMBER: 28,547
: REFERENCE/DOCKET NUMBER: 89-97
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 499-8080
: TELEFAX: (303) 499-8089
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2542 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Oryza sativa
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 453..2282
: US-08-941-445A-6

```

[illegible]

Db	1300	CCGAGAGGTTTCAGGTCATCCTTCGATTTCATCAGCGGATGAC-----	1343
QY	629	CCACCCCCATGGAGGAGGACGAGAAGCCCGCTACGGGGAAGACCTACAAGAAGATCA	688
Db	1344	-----ACGCGGTGGAGGCGAGGATCA	1368
QY	689	ACTGGCTGAAGGTGGCAATTATCCGCCGCCACAAAGCTGTGACTGTCTGCCCAACTACG	748
Db	1369	ACTGATGAAGGCCGGAATCCTGGAAGCCGACAGGGTGCTCACCGTGAGCCCGTACTACG	1428
QY	749	CGACCAGATCGCTCGCGATCCGCCGCGGTGTGAGCTGGACACGCTCATCCGCGCCA	808
Db	1429	CCGAGAGCTCATCTCCGSCATCCCAAGGGATGCGAGCTCGACAACATCATCGCGTCA	1488
QY	809	AGGGCAITGAGGCGATTGAAAGCGCATGACATTTAGGAGTAGTGGAAACCCCAAGACCGACA	868
Db	1489	CCGGCATCACCGGCATCGTCAACGGCATGACGCTACGAGTAGTGGATCTCTAGCAAGGACA	1548
QY	869	AGTTCCTGCTCGCCCTACGACCAACAGCGCTACGCCGCGAAGGCCGCGCCAGG	928
Db	1549	AGTACATCACCGCAAGTACGACGCAACCGCATCGAGGCGAGAGGCGCTGAACAAGG	1608
QY	929	AGGCCCTGCAGGCCGAGCTGGGCCCTGCCCTGTGACCCCAACGCCGCCCTGTTCGCGTTCA	988
Db	1609	AGGCGTTGCAGCGGAGCGGGTCTTCGGGTGCACAGGAAAATCCCACTGATCGCGTTCA	1668
QY	989	TCGGCGCCTTGAGGAGCAGAGGGTGTGGACATCATCTCTGCGCGCTTGCCTCAAGATCC	1048
Db	1669	TCGGCAGGCTGGAGGACAGAGGGCCCTGAGCTCATGCGCGCCGATCCCGGAGCTCA	1728
QY	1049	TGGCCACCCCAAGGTGCAAGTATCGCCATCCTGGGTACCGGCAAGGCGCTACGGAAGC	1108
Db	1729	TG----CAGGAGCAGCTCCAGATCGTTCTTCTGGTACTGGAAGAGAAGATTCGAGAAGC	1785
QY	1109	TGGTGAACGCCATCGGCACCAAGTACAGAGGCGCGCCCAAGGCGTGGTCAAGTCTCGG	1168
Db	1786	TGCTCAAGAGCATGAGGAGAAAGTATCCGGGAAGGTGAGGCGGTGGTGAATTCAACG	1845
QY	1169	CGCCCTTGCGGCACATGCTACCGCGCGCGACATTCATGTTGTCGCTCGCGCTTCG	1228
Db	1846	CGCCCTTGCTCATCTCATCATGCGCGAGCCGACGTGCTCGCGCTCCCGACGCGTTG	1905
QY	1229	AGCCTTGGGCTTGATCCAGCTGCAAGCCATCACTACGTTACCGTGCCTGGTGGTACCT	1288
Db	1906	AGCCTTGGACTCATCAGCTGCAAGGGATGAGATACGGAACGCCCTGTGCTTGGCGCT	1965
QY	1289	CCACGGCGGCTGTGTGCACACCGTCAAGGAGGCGTACCCGGCTTCACATGGGCGCC	1348
Db	1966	CCACGGTGGGCTGTGGACACGGTCTCAGAAGGCAAGACTGGTTCCACATGGGCGGTC	2025
QY	1349	TGAACCCCGAC-----AAGCTGGACAGGCTGAGCGCGACGCCCTGGCGGCACCGTGC	1402
Db	2026	TCAGCGTCCACTGCAAGGTGGTGGAGCAAGCGCATGAAGAAGGTGGCGGCCACCTCA	2085
QY	1403	GCGGTGCCAGCGAGGTGTTGGCGCGCGCTACCCCGAGATGTGGCGCTCACTGCATCA	1462
Db	2086	AGCGGCCATCAAGGTCTGCGCACCGCGGGGTACGAGGAGATGTTCAAGAACTGCATGA	2145
QY	1463	GCCAGGACTTCTCTGTGTCCAAAGCCCGCCCAAGTGGAGGCGCTGCTGGAGGAGGTG	1522
Db	2146	ACCAGGACTTCTCTGGAAGGGCTCGGAAGAACTGGGAGAACTGCTCTGGGCGCTGG	2205
QY	1523	TGTACGCAAGGGGCGGTGGCCACCG	1549
Db	2206	GCCTGCGCGGACGCGCGCGGGGATCG	2232

RESULT 3
US-09-388-743-21
; Sequence 21, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:

```
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Tulipa fosteriana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58)...(1857)
; US-09-388-743-21

Query Match      14.1%; Score 276.2; DB 4; Length 2067;
Best Local Similarity 51.9%; Pred. No. 7.5e-40;
Matches 820; Conservative 0; Mismatches 663; Indels 96; Gaps 5;

QY 1 GCGGTGACATCGTGTGCTGCTGAGTGCCTTGGTCCAGAGCGGGCGGCTG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 GGGATGAACCTGCTGCTCGGACCGGAGACGGGTCCGTACAGCAAGCGCGGCTC 330

QY 61 GCGCATGTGACTGGTGCCTTATTGAGTGTCAAGCGCGGCCACCGGTCAAGACC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 GGGATGTGTAGAGGGTTACCGCCCGCCCTGCGCGGAGAGGGCATCGGTCAIGTT 390

QY 121 ATTGCCCTCGCTACGACCACTAGCTGAGCGCTGGGACACCTCGGTGGTGGACATC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 GTCACCTCGCGGTACGATCAGTACAAGGATGATGATGATGATGATGATGATGATG 450

QY 181 ATGGCC -----GAGAGGTCGGTCTTCCATCCATCAAGAGGGGCTGCAC 228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 AAAGTCGGGGATAAAATGGAGACGGTTCGTTTCTCCACCTCCATAAGAGGGGGTGGAT 510

QY 229 CGCGTGTGGATTGACACCCCTGCTGCTGGCCAAAGTCTGGGCAAGACCGGCTCCAAG 288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 511 AGGTGTTTATGATACCCCTGCTTCTTGAGAAGGTTTGGGGAAACCGGTGGGAAA 570

QY 289 CTGTACGCGCCCTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 571 TTGTATGCTGCTGTTACTGGAACCTGATGATGATGATGATGATGATGATGATGATG 630

QY 349 TGCAGCGCGCTATGAGGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 631 TGTCAAGGCTGTTTGGAGGCTCCAGAGTCTTAATCTCAACACAGTAATATTTTCT 690

QY 394 -----GGCAGGACTGCTGCTTCTGCGCCCAACGACTGGCCTCGCCCTGGTGCC 444
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 691 GGACATATGCTGAAGATGCTGTTTATTCGAACGATGGCAGCTGGACCTCTTCCA 750

QY 445 GTCTGCTGAGGAGGAGTACAGCCCAAGGCGCAGTTACACAGGCGCAAGTCGCTG 504
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 751 TGTACTTGAAGAGTGTATATAATCAAGAGGATATATAGAGTGTGCAAGGTTGCC 810

QY 505 GCTATCCACATCGCTTCCAGGCGCATGTGGAGGAGGCTTTCAGGACACGAAG 564
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 811 TGCATTCATATATGGCATACAGGCGAGATTCGCTTCTGATGATTCGCTCTCAAC 870

QY 565 CTGCCCCAGGCGGCTTTGACAAGTGGCTTCTGCGGACGCTATGCGCAAGTTCAC 624
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 871 CTTCCAGACACATTTAAATCTCGTTTATTCGATGATGATGATGATGATGATGATG 924

QY 625 GAGGCCACCCCATGGAGGAGACAGAGAGCCCGCTGACGGGAAACACCTACAGAG 684
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 925 -----GTGAAAGGTAGAAA 939

QY 685 ATCAACTGGCTGAAGGTTGGCATTATCGCGCGGACAGGCTGGTGAAGTGTGCGCCCAAC 744
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 940 ATAAATTGGATGAAGGCTGGAATATTTGAAGCGGACACTGTGTAACTGTGAGCCCGTAT 999
```

```
QY 745 TAGCGACCGAGATTCGCTGCGATGCCCGCGGCTGAGAGCTGGACACCGTCAATCCGC 804
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1000 TATGCTTAAGAGCTGCTGCTTGGAGAAAGATAGAGTGTGAGAGTGTGAGTGTCTCGC 1059

QY 805 GCGAAGGGCAITGAGGCGCATGTGCAAGCGCATGACATTTAGAGAGTGAACCCCAAGACC 864
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1060 TTGAGGGGCGTCAAGGAATTTGATGGATGATGATGATGATGATGATGATGATGATG 1119

QY 865 GACAAGTTCTGCTGCTGCGCCTACGACAGAACAGCTGTACGCCGCAAGCGCGCGCC 924
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1120 GACAAATTTATCACTGCAATTTAGATGCAACATTTGTAACAGGCAAAACGTTTAA 1179

QY 925 AAGAGGCGCTGCGAGCGGAGCTGGCGCTGCTGTGACCCACCGCGCCCTGTTGCC 984
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1180 AAGCAAGAATTTACAAGCAGAAAGTTGGCTTGCTGTAGATCCAGACATTTCTGTATAGTT 1239

QY 985 TTATCGCGCCCTGGAGGAGCAGAAAGGTTGGACATCATCTTGGCGCCCTGCCCAAG 1044
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1240 TTTGTTGGAAGGCTGGAGGAGCAGAAAGTTTCAGATATTTAGCTGACGCAATTTCCAGAA 1299

QY 1045 ATCTGTGCCACCCCAAGGTGCAGATGCCATCTCTGGGTACCGGACGCGCGCTACGAG 1104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1300 TTAATGG---ATGAGAACGTTTCAGATCATATTTCTTGAACCTGGCAAGAACACCTCGAA 1356

QY 1105 AAGTGTGTGAACGCGCATCGGCACCAAGTACAAAGGCGCGCGCCAGGGCGTGGTCAAGTTC 1164
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1357 AAGGAGCTTGAAGAAATAGAAACAAATTTCCAGACAGATGAGACTTTGTCGAAAATTC 1416

QY 1165 TCGGGCGCCCTGGCGCACATCTCACCGCGCGCGGACITTCATGCTGGTGCCTCGCGC 1224
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1417 AATGTTGCGTTGGCTCATATGATGATGCTGGAGTGATTTTATAATTTCCCTAGTAGA 1476

QY 1225 TTCAGAGCCTCGCGGCTGATCCAGCTGCACGCCATGCACTACGGTACCCTGCCCTGGTA 1284
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1477 TTTGAGCGCTGGGCTTATTCAGCTTGAAGCATGAATATGGGATGCCAGCCATATGT 1536

QY 1285 GCTTCCACCGCGCGCTGCTGCACACCTCAAGAGGCGCTCACCGGCTTCCACATGGC 1344
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1537 TCCAGCACCGGTGCTTGTGTAGACACAATCAGGAGAGCTTCCCGGATTTTCAACATGGT 1596

QY 1345 GCGCTGA-----ACCCCGCAAGCTGGACGAGGCTGACGCGGACGCGCTGCGCCGCCACC 1398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1597 GCTTCACTGTTGAGTGTGAACCTGTTATCCGGTGGATGTTGGCGGATTTGTTAAACT 1656

QY 1399 GTGCGCCCTGCGAGGAGTGTGTTGCGGCGCGCCCTACCCCGAGATGTTGCGCCAACTGC 1458
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1657 GTAAAGAGGCGCTTAAAGTCTATGGAATCCAGCTTCCAGGAAATGTTTTCAGAACTGC 1716

QY 1459 ATCAGCAGGAGCTGCTGCTGTCAGGCGCGCGCCGCAAGTGGAGGCGCTGCTGGAGGAG 1518
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1717 ATGGTCAAGATCACTCATGGAAGGAACTGCAAAATAATGGGAAGACTACTCTCTGGA 1776

QY 1519 GTGGTGTACGCAAGGCG 1537
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1777 CTGGAAGTCAGCGCAGCG 1795
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 4
US-09-388-743-17
; Sequence 17, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
```

```

; LENGTH: 2274
; TYPE: DNA
; ORGANISM: Typha latifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)...(1956)
US-09-388-743-17

Query Match      13.7%; Score 266.6; DB 4; Length 2274;
Best Local Similarity 52.9%; Pred. No. 3.5e-38;
Matches 828; Conservative 0; Mismatches 639; Indels 98; Gaps 8;

QY 1 GCGTGGACATCGTATGGTTGCTGCTGAGGTGCGCCCTTGGTCCACAGCGGGCGCTG 60
Db 373 GGGATGAACCTAGTCTTTGGAGCTGAGATGGCTCCATGGACGAACACCTGGAGCCCT 432
QY 61 GCGCATGTGACTGTGGCTGCTATTTAGCTGGTCAAGCGCGGCCACCGGCTCATGCC 120
Db 433 GGTGATGTTCTTGGAGGACTCCACCGGCATTTGGCGGCAATGGACATCGAGTTATGTT 492
QY 121 ATTGCCCTCGCTACGACAGTACGCTGACGCTGGACCTCGGTGGTGGTGGTGGTGA 179
Db 493 ATACGCCACGTTATGATCAATATGATGATGCTTGGGATACAGATGCTCTTTGAGTTG 552
QY 180 -----CATGGCGGAGAGGTCCGCTACTTCCACTCCATCAAGAAGGGCGTGAC 228
Db 553 AAAGTTGGGATAGGTGTGAACCGTGGCTTCTTCACTGCTATATAAGAGGAGTTGAT 612
QY 229 CGGTGTGGATGACACCCCTGTTCTGCGCAAGTCTGGGCAAGACCGGCTCCAAAG 288
Db 613 CGAGTTTTCGATACCCCTATGTTTCTTGGAGGCTGTGGGGAACACTGTGGGAAG 672
QY 289 CTGTACGCGCCCGCTCGCGGCTGACTACTGTGACACACACAGCGCTTGGCCCTGTT 348
Db 673 ATTATGGTCTTACATGTGAACAGACTACAGACAAATCAGTACGCTTTCAGCTTTCTA 732
QY 349 TGAAGGCGCTATTTAGGCTGCGCGGCTGCTGCGCTTGGCCCTTGGCCCTTGGCCCT 393
Db 733 TGGCAGGACGATTTGGAAGTCTTAGAATTTCTAAATCTCAACACAGTATCTTCTCT 792
QY 394 -----GGCGAGGACTCGCTTCTGCGGCAACGACTGGGACTCGGCCCTTGGTCC 444
Db 793 GGTCTTTAAGGAGATGTTATCTTCAATTTGCAATGATTGGCACACTTCTTCTGCCA 852
QY 445 GTCTGTCTGAAGGACGAGTACCGGCCCAAGGCCAGTTCCACCAAGCCAGTCGTCTG 504
Db 853 TGCTACTTAAAGAGATGTACCATCCCGTGGCATTTACAGAACGCCAAGGTTGTTTC 912
QY 505 GCTATCCACACATCGCTTCCAGGCGCGCATGTGGAGGAGGCTTTCAAGGACACGAAG 564
Db 913 TGCATTCACAATATATACATCAAGTCGATTTCTCCCTCAGACTTCGAATTTCTCAAT 972
QY 565 CTGCCCCAGGCCCTTTGACAGCTGGCCTTCTCGAGCGGCTATGCCAAGGTTTACACT 624
Db 973 CTTCGGAG-----AATTTCAAAATCT 993
QY 625 GAGGCCACCCCATGAGGAGGACGAGAACGCCCTCGCTGACGGGAAAGACCTACAAGAG 684
Db 994 TCTTTTCAGTTTCATGATGGTTACACAGCC-----TGTGAAGGAAATGAAG 1041
QY 685 ATCACTGCTCAAGGTTGGCATTTATCGCGCGGACAAAGCTGTGTGACTGTGTGCGCCAA 744
Db 1042 ATAAATTTGATGAAGCAGGAATCTTAGAATCAGACAGGTTTACAGTGTGATCCATAT 1101
QY 745 TAGCGACCGAGATCGCTGCCGATCGCGGCGGTGTGGAGTGGAGTGGACCGTCACTCCG 804
Db 1102 TATGCACAGAGCTCTTTACAGAGAAGAAAGGGAGTCTGAGTTGGACACATTTTGCCT 1161
QY 805 GCGAAGGCGATTGAGGCGATTGTGAACGCGCATGGACATTTGAGAGTGGACCCCAAGACC 864
Db 1162 GTGACCAAGTATCACAGGAATTTGAATGGAATGGATGTTAAATGAGTGGAAATCCATTA 1221
QY 865 GACAAGTTCTCTGTCGGCCCTTACGACCAAGAACAGCGTCTACCGCGCAAGCGCGCCG 924

```

```

Db 1222 GACAAAGTATATTTCTGTTAATATGATGCAAAACCTGTATGAAAGCAAGCTCTTAAC 1281
QY 925 AAGGAGGCGCTCGCAGGCGG-AGCTGGCGCTGCTGTGGACCCACCGCCCCCTGTTCGC 983
Db 1282 AAGGAGCATTGCAAGCTGAAAGTTGGCTTGGCTGTGAGACAGGACATCCCTGTATTT 1341
QY 984 CTTTCATCGCCCGCTTGGAGGAGCAGAAAGGTTGTGACATCATCTTGGCGCGCTTGC 1043
Db 1342 ATTTCAT-GGAAGCTAGAGGACGACAAAGGATCATATTTAGCAGCATCATCCAGA 1400
QY 1044 GATCTGTGCCCGCCCGCAAGGTGCAGATCCCATCTCGGTACCGCAAGCGCGCTTACGA 1103
Db 1401 GATCATGG---ATGAGAATTTTCACTAATTTCTTGGAACTGCAAGAGGAAATGGA 1457
QY 1104 GAAGCTGTGAACGCGCATCGGCCACCAAGTACAAAGGCGCGCCGCAAGGGGTGGTCA 1163
Db 1458 GAATCAGCTTGAGAGTATGGAGGAATGTTCGCCGACAAAGTGTGGGCGAGTTATGA 1517
QY 1164 CTCGCGCGCCCTTGGCGCACATGCTCACCGCGCGCGCGCTTCACTGCTGGTGCCTCG 1223
Db 1518 CAATGCTCCCTTAGCTCACCAGATGACGCGGGAGCTGATATAATTTGATTCATCCAA 1577
QY 1224 CTTGAGCGCTTGGCGCTGATCCAGCTGCACGCCATGCACGTACCGTACCGTGGCG 1283
Db 1578 ATTGCAACCATCGCGCTTATCCAGTTGCAAGGCTCAATATGAAAGCGCTTCTGCGTG 1637
QY 1284 AGCCTCCACCGCGCGCTGTGTCACCGCTCAAGGAGGCGGTCAACCGCTTCCACATGG 1343
Db 1638 TTCTCTCACTGTGGCTTGTGGACACGCTGAAAGAGGCAAACTGGATTCATATGG 1697
QY 1344 GCGCCTGA-----ACCCGACAAAGCTGGACGAGCTGACCGCGCGCTTGGCGCG 1397
Db 1698 ACCTTTTCACTGCTGAATGCGAAGTGGTCTTCTTCTGATGTAAGAAAGTTGTCACA 1757
QY 1398 CGTGGCGGCTGCGCAGGAGTGTGCGGGCGCGCGCTTACCCCGAGATGTTGGCGCA 1457
Db 1758 TGTGAAAGCGGCACTTAAGGTCATCGGCACACCTTGGCTTTGAGGATATGATCAAGA 1817
QY 1458 CATCAGCAGGAGCTCTCTGCTCCAGCGCGCGCGCGCTTACCCCGAGATGTTGGCG 1517
Db 1818 CATGGCACAGACCTCTCATGGAAGGCGCTGCAAAAGACTGGGAGCAAGTTCTACTGA 1877
QY 1518 GGTGG 1522
Db 1878 CTTGG 1882

```

RESULT 5

```

US-09-388-743-13
; Sequence 13, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2176
; TYPE: DNA
; ORGANISM: Canna edulis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)...(1928)
US-09-388-743-13

```

```

Query Match      13.3%; Score 259.6; DB 4; Length 2176;
Best Local Similarity 51.6%; Pred. No. 5.6e-37;

```

Matches 795; Conservative 0; Mismatches 649; Indels 96; Gaps 5;

QY 5 TGGACATCGTATGTTGCTGCTGAGTGGCGCCCTTGGTCCAAAGAGCGGCGCTGGCG 64
Db 349 TGAACCTGGTGTGTTGTTGTTGAGGTAGCTCCATGGAGCAAAAGTGGGGCCCTGGCG 408
QY 65 ATGTGACTGGTGGCTTCCTATGCTGCTCAAGCGCGCCACCGCTCATGACCATG 124
Db 409 ATGTCTTGAAGGATGCTCCACCTGCTATGCTGCTCAATGGGCACAGGTCATGACCGTGG 468
QY 125 CCGCTCGTACGACCACTAGCTGAGCGCTGGGACACCTGGGTGGTGGACAT----- 179
Db 469 TGGCAGCATACCAATAAAGATATCTGGGATCAAGTGTCCAGTGTGAGTTAAAG 528
QY 180 -----CATGGCGAGAGGTCCTGCTTCCACCTCCATCAAGAGGGGTGACCGG 232
Db 529 TTGGGATAGATGAACTGTCCTGCTTCCACCTGCTACAAAGGGGATGATCGGG 598
QY 233 TGTGGATTGACCAACCGCTGCTTCCGCAAGCTCTGGGCAAGACCGGCTCCAAAGCTGT 292
Db 589 TTTTGTGGATCACCTATGTTTTCGAGAAGGTTTGGGGGAAACAGAGGAAATAT 648
QY 293 ACGGCGCGCTCGGCGCTGACTACTGGAACAACACAGCGCTTCGCCCTGTTGCA 352
Db 649 ATGCTCTGTTACAGGAACAGATATGACAGCAATCAACTTAAGATTACAGCTTTTGCC 708
QY 353 AGCGCGCTATTGAGGCTGCGCGTGTGCTGCTTCCGCGCGCGGAGACTGC----- 405
Db 709 TGGAGCTCTGGAAGCTCCAGACTCTTAATCTCAACACAGCAATATCTTCGGAC 768
QY 406 -----GTCTGCTGGCCAAAGCTCTGGGCAAGACCGGCTCCAAAGCTGT 508
Db 829 ACTTGAAGAACTATGACCAATACATGATTTACATGAATGCTAAAGTTGCAATTTGCA 888
QY 509 TCCAAACATCGCTTCCAGGCGCGCATGTGGGAGAGGCTTCAAGGACACGAGCTGC 568
Db 889 TTCAATATATGTTACAGGCGCGATTTGCTTTTCGGACTTTGAATCCTTAATCTCC 948
QY 569 CCCAGGCGCTTTGACAAGCTGCGCTTCTGGAGCGGTATGCCAAGTTTACACTAGG 628
Db 949 CCAATAAATTTAAATCTTCATTTGATTTGATGATGATGATGACAAACT----- 998
QY 629 CCACCCCATGAGGAGGACGAGAGCGCCGCTGACGGGAAAGACCTTACAGAGATCA 688
Db 999 -----GTGAAGGAAGGAAATAA 1017
QY 689 ACTGGCTGAAGGTGGCATATGCGCGGACAAAGCTGGTACTGTGTGCGCCCACTACG 748
Db 1018 ATTGGATGAAGCTGGATATAGATGATAGTGTGATAGTGTGCTGACCGTGAGCCCATATG 1077
QY 749 CGACCGAGATCGCTGCGGATGCGCGCGCTGTGGAGCTGGACACCGCTCATCGCGCA 808
Db 1078 CCCAAGAGCTGTCTCAGGGGTAGAGAAGGTTGTAGTTGGCAATATCTCGGCATGA 1137
QY 809 AGGCGATTGAGGCACTTGTGAACGCGATGAGCATTTGAGAGCTGGAACCCCAAGACCGACA 868
Db 1138 AAACACTCTGGAATAGTAATGGAATGGAGTGGACCCACCGAGTGGATCCATTAACAGACA 1197
QY 869 AGTTCTCTGCGCGCTTACCAACAGAACAGCTGTACGCGGCAAGCGCCCGCAAG 928
Db 1198 AATATATTTACAAACTACCATGCAACACTGATTTGATGATGCAAAACCTCTCTGTAAGG 1257
QY 929 AGGCGCTGACGCGAGTGGCGCTGCTGTGGACCCCAACCGCCCTGTTGCGCTTCA 988
Db 1258 AAGCTTTGCAAGCTGAGTGTGGCTGCTGTTAAACAAAACAAAGCTTTGTTGGCCTTG 1317
QY 989 TCGCGCGCTTGAGGAGCAGAGGTTGTGGACATCATCTCGCGCGCTGCGCAAGATCC 1048
Db 1318 TTGAAGACTAGATGAGCAGAAAGGCTCAGACATCTAGCTGACCAATTCAGACATTC 1377

QY 1049 TGGCCACCCCAAGGTGACATCGCCATCTCTGGGTACCGGCAAGGCGCCCTACAGAAC 1108
Db 1378 T---TTGTGAGATGTTCAAGTGTATGACTTGTGCACTGCAAGAGAGTGTGAGAGTG 1434
QY 1109 TGTGAACGCCATCGGACCAAGTACAGGCGCGCCCAAGGCGGTGTTCAAGTTCCTCG 1168
Db 1435 AACTTACATTACTTTGAGGAAATGTTTCCAGACAAATTCAGAGCACATCTCAAATTCACG 1494
QY 1169 CGCCCTGGCGCACATCTCACCGCGCGCGGCTTCATCTGCTGGTCCCTCGCGCTCG 1228
Db 1495 TTCTTTAGCTGATGCAATCATGCGAGGACTGATATCTTGTATTTCAGAGCATTCG 1554
QY 1229 AGCCCTCGCGCTGATCCAGCTGACGCCATGACCTACCTACCTACCTGCGGCTGACCT 1288
Db 1555 AACCTGTGCGCTCATTCAGCTTCAGGCCATGCGATATGGAACCTCTCCCTATGTGTAGCA 1614
QY 1289 CCACCGCGCGCTGCTGACACCGTCAAGGAGGCGCTCACCGGCTTCCACATGGCGGCC- 1347
Db 1615 CCACTGTGAGCTGTTTGACACACGTCAAGAGGCTTCACTGGCTTCCATATGGCGCCCT 1674
QY 1348 -----CTGAACCCCGCAAGGTGACGAGGCTGACCGGAGCGCTTGGCGGCCACCGTGC 1402
Db 1675 TCACTGTGAGCTGTGATCCGCTAGACAAAGCTGATGTACAAAGATTTCTCGAAACACGA 1734
QY 1403 GCGGTGCGAGGAGTGTGTTGGGCGCGCGCTACCCGAGATGTTGGCCCAACTGCATCA 1462
Db 1735 AAGGCGCTCAAAAGTCTATGSAACACCTGCTTTTGTGGAGATGATCAAGAACTGCATGA 1794
QY 1463 GCCAGGACCTGCTGCTGCCAAGCGCGCCCAAGAGTGGGA 1502
Db 1795 ACCAAGATCTCTATGNAAGGACCTGCAAAAGAGTGGGA 1834

RESULT 6
US-09-388-743-1
; Sequence 1, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: Curcuma zedoaria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (130)...(1974)
US-09-388-743-1

Query Match 13.1%; Score 255.4; DB 4; Length 2202;
Best Local Similarity 51.8%; Pred. No. 3e-36;
Matches 799; Conservative 0; Mismatches 646; Indels 96; Gaps 6;

QY 5 TGGACATCGTATGTTGCTGCTGAGTGGCGCCCTTGGTCCAAAGAGCGGCGCTGGCG 64
Db 395 TGAACCTGATCTTTGCTGCTGAGTGGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 454
QY 65 ATGTGACTGGTGGCTGCTGCTGATGCTGCTCAAGCGCGCCACCGCTCATGACCATG 124
Db 455 AHTTCTTGGAGTTTGGCCCGGCTGCGGCAAGGACACAGGCTGATGACTATAG 514
QY 125 CCGCTCGTACGACCACTAGCTGACCGCTGCGGACACCTCGGTGGTGGTGGACATCATG 184
Db 515 CACCGCGACATGACCAATACAAAGATGAGTGGATACGGCTGCTTCTTGTGAGTTGAAAG 574

QY	185	-----GCGAGAAGTCCGGCTACTTCCACTCCATCAAGAAGGCGTGACCGG	233
Db	575	TTGGTGTATAGAATTTAAACTGTTTCGCTTTTCCACTCCACAAAAGGAGTTGATCGG	634
QY	233	TGTGGATTGACCAACCCCTGGTCTCTGCGCAAGCTGTGGGCAAGACCGGCTCCAAAGCTGT	292
Db	635	TGTTTGTGGATCACCCCTCTCTCTCTTGAGAAGGTTTGGGAAAAAATCTGGAGAAAGATAT	694
QY	293	ACGGCCCCCGCTCCGGCGCTACTACCTGTACACCAACACAAAGCGCTGCGCCCTGTCTGCA	352
Db	695	ATGCTCTGTGCACAAGAACTGATATGAAGACAACCAAGCTAAGGTTCTGTCTTCTGTGTT	754
QY	353	AGGCGCGTATGTAGGCTGCCCGGTGTGTG-----CCCTTCGGCG	391
Db	755	TGGCAACTCTGGAACATCCAAGGTTCTGAATCCCAACAATACAAATATCATTTCTGGAC	814
QY	392	CCGCGGAGGACTGGTCTTCGTGGCCAAACGACTTGGCACTTCGGCCCTGTGTGCCGCTCTGC	451
Db	815	CAAAAGTGTGAAGATTTATTCATTCGTAAACGATTTGGCATCTGCTCTATTACCTTGCATT	878
QY	452	TGAAGGAC---GAGTACCAAGCCCAAGGGCCAGTTTCAACCAAGCCCAAGTCGGTCTGGCTA	508
Db	875	TAAAGACCATGTTATATCAAGCCCATGGAATATACAAAAATGCTAAAGTTGTTTCTGCA	934
QY	509	TCGACAACATCGCTTCCAGGGCCGATGTGGAGGAGCGCTTTCGAAGCACAGAAGCTGC	568
Db	935	TTCAATAATTTGGGTATFACGGGACGGTTTGCCCTTTGAAGATTTTTCGGCTCTCAATCTCC	994
QY	569	CCCAGGCGCCTTTGACAAGCTGGCCCTCTCGSACGGCTATGCCAAGGTTTACATCGAGG	628
Db	995	CTGATACATTTCAAGTCCTTTTGTATTCTCATGATGGCTATGCAAA-----	1040
QY	629	CCACCCCATGTGAGGAGGACGACAGACCCCGCTGACGGGAAGACCTACAGAAGATCA	688
Db	1041	-----ACCAATAAAGAGGAATAATCA	1063
QY	689	ACTGGCTGAAGGTGGCATTTATCGCCGCGACAAAGCTGGTGACTGTGTGCCCAACTACG	748
Db	1064	ACTGGATTGAAGCGGGAATTTAGAAATCATAGATCGTGCATTGACTGTGAGCCCACTATG	1123
QY	749	CGACCCGAGATCGCTGCGGATGCGCGCGGCTGTGGAGCTGGACACCGCTATCCGCGCA	808
Db	1124	CCAGGAACTGCTCTCAGGAATGATTAAGGGCGTCGAGTTGGACAATATACTTGGCGCTTA	1183
QY	809	AGGGCATTTAGGCGATTGTGAACGGCATGGACATTTGAGGAGTGGAAACCCCAAGACCGACA	868
Db	1184	AAACCATCTGTGGCATCATAAATGGAATGGACACCAACGAGTGGAAATCCCTCACAGACA	1243
QY	869	AGTTCTGTCTGCGCCCTACGACCACAGACAGCTCTACGCGGCAAGCGCGCCGCAAGG	928
Db	1244	AATACATACAGCAAAATACGACGCAACCACTGTAAATGGAGCAAAAGCCATCAACAAGG	1303
QY	929	AGGCCCTGACGGCCGAGCTGGGCGCTGCTGTGGACCCCAACCGCCCTGTTCGCCCTTCA	988
Db	1304	AAGCTTTGCAAGCTGAGTTGACTTGGCGTCAACAGTAAATCCCTGTGATAGCTTTCA	1363
QY	989	TCGGCGCCTTGGAGGACAGAGGGTGTGGACATCATCTTGGCGCGCCCTGCCCCAAGATCC	1048
Db	1364	TTGGCAGACTAGAAGAACAAGAGGTTTCAGACATCTTACGTGAAGCAATTTCCAAGTTCT	1423
QY	1049	TGSCCAACCCCAAGTGTGAGATGCGCCATCTGGGTACCGGCAAGCGCGCCCTACGAGAAGC	1108
Db	1424	T---CGATCAGGATGTTCAAGTCATAGTTCTCGGTACTGTGTGTGTGTATCTTGTATTTCCAGTAGGTTTCG	1480
QY	1109	TGTTGAACGCGCATGCGCACCAAGTACAAGGCGCGCCCAAGGCGTGGTCAAGTTCTCGG	1168
Db	1481	AACTTGCATTGCTCGAGGACAGAGTTTCCACAGCAAAATTCAGAGCTCATATGAAGTTCAATA	1540
QY	1169	CGCCCTTGGCGCACATGCTACCGCGCGCGCGGACTTCATGCTGGTGCCTTCGGCGCTTCG	1228
Db	1541	TTCCCTTTGGCTCATGGAATCATGGCGGGTGTGATATCTTGTATTTCCAGTAGGTTTCG	1600
QY	1229	AGCCCTGCGGCGCTGATCCAGCTGCAGCCGATGCACACTACGGTACCGGTGCGCGTGTAGCCT	1288

DB	1601	AACCATGGGTCTATTTCAGTCCAGGCGATGAGATACGGAACCCCTTCCAATGTGCACCA	1660
QY	1289	CCACCGGGGCCCTGGTCGACACCCTCAAGAGAGGGGCTCACCGGCTTCCACATGGGCGCC-	1347
DB	1661	CGACTGTGGGGCTGGTCGACACTGTCAAAGAAGGCAITACAGGTTTCCACATGGGTCCCT	1720
QY	1348	-----CTGAACCCCACAAAGCTTGAGCGGCTGACGGCAGCGCCCTGSCGCCACCCGTGC	1402
DB	1721	TCACTGTGGAGTCCGACATTCGCCGAGGCGCCAGCTGCTAAGANTGTGGAACCATGA	1780
QY	1403	GCGTGCACGAGGHTTTTGGGGCGGCGCTACCCGAGATGTTGGCCCAACTGCATCA	1462
DB	1781	AGAGAGCCCTTAGTTTATGGAACGCCCTGCTTTCGAGGAGATGATACAGAAGTGCATGG	1840
QY	1463	GCCAGGACCTGTCTCTGGTCCAAAGCCCGGCCAAGTGGGAG	1503
db	1841	CTCAAGATTTCTCTGTAAGGGGCCAGCAAAAGGAATGGGAG	1881

RESULT 7

US-09-196-390-5
: Sequence 5, Application US/09196390
: Patent No. 6307125
: GENERAL INFORMATION:
: APPLICANT: Block, Martina
: APPLICANT: Lorz, Horst
: APPLICANT: Lutticke, Stephanie
: APPLICANT: Walker, Lennart
: APPLICANT: Froberg, Claus
: APPLICANT: Kossmann, Jens
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
: TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
: TITLE OF INVENTION: SYNTHESIS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/196,390
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 196 21 588.9
: FILING DATE: 29-MAY-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 196 36 917.7
: FILING DATE: 11-SEP-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/EP97/02793
: FILING DATE: 28-MAY-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Haley, Jr., James F.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: AGEVO-9
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2825 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear

```

; MOLECULE TYPE:  CDNA to mRNA
;
; HYPOTHETICAL:  NO
;
; ANTI-SENSE:    NO
;
; ORIGINAL SOURCE:
; ORGANISM:      Triticum aestivum L.
; STRAIN:        cv. Florida
; TISSUE TYPE:   ca. 21 d Caryopses
; IMMEDIATE SOURCE:
; LIBRARY:       cDNA library in pBluescript sk (-)
; CLONE:         pTASS1
; FEATURE:
; NAME/KEY:      CDS
; LOCATION:      162..2559
; US-09-196-390-5

```

[illegible]

Db	1828	-----AGACCCCGGCATCGTCAACGGCATCGACCAATGAGTGGAAACCCCGAGG	1879
QY	833	GCATGACATTTGAGGAGTGAACCCCAAGACCGACAAAGTTCTCTGTCGCGCTTACGACC	892
Db	1879	TGGAACCCCACTCAAGTCGGACGGCTACACCAACTTCTCCTCAGGACGC-----	1929
QY	893	AGAACAGCGTCTACGCGGCAAGGCGCGCAAGGAGGCGCTCGAGCCGAGCTGGGCC	952
Db	1930	-----TGGACTCCGCAACGCGCAGTGCAGGAGGCGCTCGACGCGAGCTGGGCGC	1980
QY	953	TGCCTGTGACCCCAACCGCCCTCTTGCGCTTCATCGCGCGCTCGAGSAGCAGAAGG	1012
Db	1981	TGCAGTTCGCGCGCAGCTGCGCGCTGCTCGGGTTTCATCGCGCGCTGACGCGCAGAAGG	2040
QY	1013	GTGTGGACATATCTTGGCGCGCTGCCCAAGATCCTGGCCACCCCAAGGTGCAGATCG	1072
Db	2041	CGTGGAGATCATCGCGAGCCCTGCCCTGATCTGTG- --AGCCAGGAGCTGCAGCTGG	2097
QY	1073	CCATCTCTGGTACCGGCAAGGCGCGCTACGAGAGCTGGTGAACGCCATCGGCACCAAGT	1132
Db	2098	TGATGCTGGGCACCGGCGCGCACGACCTGGAGAGCATGCTGCAGCACTTTCAGCGGGAGC	2157
QY	1133	ACAGGCGCGCCCAAGGGCGTGGTCAAGTTCTCGGCGCCCTGGCGACATGCTCAACG	1192
Db	2158	ACCACGACAAGTGCGCGGGTGGTGGGTTCTCGCTGCGCTGGCGCACCGGATACGG	2217
QY	1193	CCGCGCGCGACTTCATGCTGTGTGCCCTCGCGCTTCGAGCCCTCGGCGCTGATCCAGCTGC	1252
Db	2218	CGGGGCGGAGCGGCTTCCTCATGCCCTCCCGGTTTCGAGCCGTGCGGGCTGACCAAGTCT	2277
QY	1253	ACGCCATCGCATAGGTACCGTCCCGGTGGTAGCCTCCACCGGGCGGCGTGGTCGACCG	1312
Db	2278	ACGCCATGGCTACGGCACCGTCCCGTCTGTCACGCGCTCGGCGCGCTCAGGGACACCG	2337
QY	1313	TCAGGAGGGCGTCAACGGGTTCCACATGGGCGCGCTGACCCCGACAGCTGSAACGAGG	1372
Db	2338	TGCGCGGCTTCGACCCCTTCAACCACTCGCGGGCTGGGTGGACGPTGACCGCGCCGAGG	2397
QY	1373	CTGACCGCGAGCCCTTGGCGCGCACCGTGGCGGTCCAGCAGGAGTGTTCGCGGCGGCC	1432
Db	2398	CGCAACAAGCTGATCGAGGCGCTCGGCGCATGCTCGGCACCTACCGAGACTTCAAGGAGA	2457
QY	1433	GCTACCCCGAGATGGTGGCCAACTCAGTCAGCAGCAGACTGCTCTCTTCCAGGCGCCGCC	1492
Db	2458	GCTGGAGGCGCTCCAGGACGCGGCATGTCGACAGGACTTCAGCTGGGAGCACCGCCCA	2517
QY	1493	AGAAAGTGGGAGGCGCTCTCGGAGGAGTGGTGTAC	1527
Db	2518	AGCTCTACGAGAGCGTCTCGTTCAGGCGCAAGTAC	2552

```

RESULT 8
US-08-941-445A-10
; Sequence 10, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```


Db 2048 ARWSNTGTMGNGCMTGYMNGCNGMNGNATGCGNGARGAYYTNWSNTGGAYCAYGCG 2107
Qy 1490 CCCAGAACTGGAGGCGCTGCTGGAGGAGTGGTGTAC--GGCAAGGGGGGGTGGCCAC 1547
Db 2108 CNGYNTWTAAGAYGNTYNTGNTAARGCNAARTAYCARTGSTRRCNAAYTRYTNG 2167
Qy 1548 CGCCAAGAGGAGGAGATCAAGGTGCCGTGGCCGAGAAGATCCCGCGGACCTCCCGC 1607
Db 2168 CNACNMGMNGMNGNWSNTGYMNGMGNACNTGGACNTYNTYNGMNGNTNTYNSYNTNG 2227
Qy 1608 CGTGTCTACGCCCCCAACACCCCTGAAGCC 1637
Db 2228 CNGCNYTNATGMNGCWNWSNCAYYTNMGM 2257

RESULT 10
US-09-345-214-20
; Sequence 20, Application US/09345214
; Patent No. 6392120
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Broglie, Karen E.
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS
; FILE REFERENCE: BB-1147
; CURRENT APPLICATION NUMBER: US/09/345,214
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 060/094,436
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; TYPE: DNA
; ORGANISM: Zea mays
US-09-345-214-20

Query Match 10.6%; Score 207; DB 4; Length 2248;
Best Local Similarity 55.1%; Pred. No. 7.1e-28;
Matches 477; Conservative 0; Mismatches 370; Indels 18; Gaps 3;

Qy 678 CAAGAAGATCAACTGGCTGAAGGTGGCAATATCGCGCGCAAGCTGGTGTGCTGTGC 737
Db 1331 CGAGCAGCGCAACATCTTTGCCGGGTCTGAAGATGGCAGACGGGTGGTGTGCTGTG 1390
Qy 738 GCCCAACTAGCGCAGCAGATCCTGCCGATCGCGCGCGGTGTGGAGCTGGACACCGT 797
Db 1391 CCSCGGCTACTGTGGAGCTGAAGACAGTGAAGCGCGGTGGGGCTCCACGACATCAT 1450
Qy 798 C---ATCCGCGCAAGGCGATTGAGGCGATTGTGAAGCGCATGGACATGAGAGTGGAA 854
Db 1451 CCGTTCTAACGACTGAAGATCAATGGCATCTGAAGCGCATGCAACCGCATGCCACGAGTGGAA 1510
Qy 855 CCCCAAGCGCAGCAATCTCTGTCTGCGCCCTACGACCAAGACAGCG-----T 902
Db 1511 CCCCAAGGTGGAGCTGCATCTGCGGTGGAGCGCTACACCAACTACTCCCTCGACACACT 1570
Qy 903 CTACGCGCGCAAGCGCGCGCAAGAGCGCTTGAAGCGCATGGACATGAGAGTGGACAT 1622
Db 1571 CGACGCTGGAAGCGGCAAGTGAAGCGCGCTTGAAGCGCGCTTGAAGCGCGCTTGAAGCG 1630
Qy 963 CCCCACGCGCCCGCTTCTGCGCTTATCGCGCGCTTGAAGCGCGCTTGAAGCGCGCTTGAAGCG 1690
Db 1631 CGACGAGCTGCGCGTCTCGGCTTCTATCGCGCGCTTGAAGCGCGCTTGAAGCGCGCTTGAAGCG 1690
Qy 1023 CATCTGCGCGCGCTTCTGCGCGCTTATCGCGCGCTTGAAGCGCGCTTGAAGCGCGCTTGAAGCG 1690
Db 1691 CATCTGCGCGCGCTTCTGCGCGCTTATCGCGCGCTTGAAGCGCGCTTGAAGCGCGCTTGAAGCG 1690
Qy 1083 TACCGCGAGCGCGCTTCTGCGCGCTTATCGCGCGCTTGAAGCGCGCTTGAAGCGCGCTTGAAGCG 1690
Db 1748 CACCGCGCGCGCGCTTCTGCGCGCTTATCGCGCGCTTGAAGCGCGCTTGAAGCGCGCTTGAAGCG 1690

Qy 1143 CCCCAGGCGGTGGTCAAGTTCTCGCGCGCGCTTCTCGCGCATGCTCACCGCGCGCGCGCA 1202
Db 1808 GGTGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1867
Qy 1203 CTTTCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1262
Db 1868 CTTTCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1927
Qy 1263 CTACGCTGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1322
Db 1928 ATACGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1987
Qy 1323 COTCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1382
Db 1988 CGACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2047
Qy 1383 CGCGCTGCGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1442
Db 2048 GATCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2107
Qy 1443 GATGTCGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1502
Db 2108 TCTCAGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2167
Qy 1503 GGGCTGCTGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1527
Db 2168 GGAGCTGCTTGTCAAGGCGCAAGTAC 2192

RESULT 11
US-09-345-214-16/c
; Sequence 16, Application US/09345214
; Patent No. 6392120
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Broglie, Karen E.
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS
; FILE REFERENCE: BB-1147
; CURRENT APPLICATION NUMBER: US/09/345,214
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 060/094,436
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Zea mays
US-09-345-214-16

Query Match 10.6%; Score 206.6; DB 4; Length 1798;
Best Local Similarity 55.0%; Pred. No. 8.1e-28;
Matches 476; Conservative 1; Mismatches 370; Indels 18; Gaps 3;

Qy 678 CAAGAAGATCAACTGGCTGAAGGTGGCAATATCGCGCGCAAGCTGGTGTGCTGTGCT 737
Db 918 CGAGCAGCGCAACATCTTTGCCGGGTCTGAAGATGGCAGACCGGTGGTGTGCTGTGCT 859
Qy 738 GCCCAACTAGCGCAGCAGATCCTGCCGATCGCGCGCGGTGGTGTGCTGTGCTGTGCTGTG 797
Db 858 CCGCGGTACTCTGGGAGCTGAAGACAGTGAAGCGCGGTGGGCGCTCCACACATCAT 799
Qy 798 C---ATCCGCGCAAGGCGATTGAGGCGATTGTGAAGCGCATGGACATGAGAGTGGAA 854
Db 798 CCGTTCTAACGACTGAAGATCAATGGCATCTGTGAAGCGCATGCCACGAGTGGAA 739
Qy 855 CCCCAGACGACCAAGTCTCTGTCTGCGCGCTTACGACCAAGACAGCG-----T 902
Db 738 CCCCAGAGTGGAGTGCACCTTGGGTGGAGCGCTTACCAACTACTCTCGTGGAGACT 679
Qy 903 CTACGCGCGCAAGCGCGCGCAAGGAGCGCTTGAAGCGCGCGCTTGAAGCGCGCTTGAAGCG 962

Db 678 CGACCTGAAAGCGGCGAGTGCAGGCGGCCCTTCAGCGGGAGCTGGGGCTTGAAGTGGC 619
QY 963 CCCACCGCCCGCTTCTGCGCTTCATCGCGCGCTTGGAGGACGAGAGGCTGTGACAT 1022
Db 618 CGACGACGCTGCGCTGCTGCGCTTCATCGCGCTTGGATGACAGAGGCGTGGACAT 559
QY 1023 CATCTGGCGCGCTTGCACCAAGTCTTGCACCGCCCAAGAGTGCAGATCCCTGGG 1082
Db 558 CATCGGGGACGCGATCGCTGGATC---CGGGGAGGAGCTGCAGCTGGTGTGATGCTGG 502
QY 1083 TACCGGACGCGCTTACGAGAGTGTGAACGCTTGAACGCTTGCACCAAGTACAAGGCGG 1142
Db 501 CACCGGGCGCGGCTTCAAGTCTTTCGCGCGCTTGGCGGCATCTGAGAGGAGGAGTCCCAACAA 442
QY 1143 CGCAAGGCGTGGTCAAGTCTTTCGCGCGCTTGGCGGCATCTGAGAGGAGGAGTCCCAACAA 1202
Db 441 GGTGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 382
QY 1203 CTTCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1262
Db 381 CGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 322
QY 1263 CTACGCTACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1322
Db 321 ATACGCGACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 262
QY 1323 CGTACCGGCTTCCATGCGCGCTTGAACCGCGCTTGAACCGCGCTTGAACCGCGCTTGA 1382
Db 261 CGACCGCTTACGAGCGCGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 202
QY 1383 CGCGCTGGCGCGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1442
Db 201 GATCGAGGCGCTACGCGCTTGCACACGCTACCGAGAGCTACGAGAGAGTGGG 142
QY 1443 GATGGTGGCACTGATCAGCAGCGCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1502
Db 141 TCTCAGCGCGCGCTGATGCTGAGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 82
QY 1503 GGGCTGCTGGAGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1527
Db 81 GGAGCTGCTTGTCAAGGCGCAAGTAC 57

RESULT 12
US-09-345-214-15
; Sequence 15, Application US/09345214
; Patent No. 6392120
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Broglie, Karen E.
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; FILE REFERENCE: BB-1147
; CURRENT APPLICATION NUMBER: US/09/345,214
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 060/094,436
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Zea mays
US-09-345-214-15

Query Match 10.6%; Score 206.6; DB 4; Length 2019;
Best Local Similarity 55.0%; Pred. No. 8.2e-28;
Matches 476; Conservative 1; Mismatches 370; Indels 18; Gaps 3;

QY 678 CAAGAAGATCAACTGGCTGAAGAGTGGCATTTATCGCGCGCGAGAGCTGGTGGTGGTGGTGG 737
Db 887 CGAGCAGCGCAACATCTTTGCGCGGGGTCTGAAGATGCGAGACCGGGTGGTGGTGGTGG 946

QY 738 GCCCACTAGCGGACGAGATCGCTGCCGATGCCGCGCGGTGTGGAGTGGACACCGCT 797
Db 947 CCGCGCTTACCTGTGGAGCTGAAGACAGTGAAGGCGGCTCCACACATCAT 1006
QY 798 C---ATCCCGCGCAAGGCAATTGAGGCAATTGTGAACGCGATGACATGAGAGTGGAA 854
Db 1007 CCGTTCTAAGCATGCAAGATCAATGGCATCGTGAACGCGATGACACGAGGAGTGGAA 1066
QY 855 CCCAAGACCGCAAGTCTTCTGCTGCGCTTACGACGACGAGAGAGG---T 902
Db 1067 CCCAAGTGGAGCTACCTGCGGTGCGAGCGCTACACCAACTACTCCCTCGAGACACT 1126
QY 903 CTACGCGCGCAAGCGCGCCCAAGGAGGCGCTGAGGCGGAGCTGGCGCTGCTGTGGA 962
Db 1127 CGACGCTGAAAGCGGAGTGAAGGCGGCTGAGCGGAGCTGGCGCTGGAAGTGG 1186
QY 963 CCCACCGCGCGCTTTCGCTTTCATCGCGCGCTTTCGAGGAGGAGGAGGAGTGGACAT 1022
Db 1187 CGACGAGTGGCGCTGCTGCGCTTTCATCGCGCGCTTTCGAGGAGGAGGAGGAGTGGACAT 1246
QY 1023 CATCTGGCGCGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGGAGTGGG 1082
Db 1247 CATCTGGCGCGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGG 1303
QY 1083 TACCGCGCAAGCGCGCTTACGAGAGGCTGAGCGCGCTTTCGAGGAGGAGGAGTGGG 1142
Db 1304 CACGCGCGCGCTTTCGCGCGCTTTCGAGGAGGAGGAGTGGGAGGAGTGGGAGGAG 1363
QY 1143 CGCAAGGCGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGGAGGAG 1202
Db 1364 GGTGCGCGGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGGAGGAG 1423
QY 1203 CTTCATGCTGGTGGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGG 1262
Db 1424 CGTGTGGTGGTGGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGG 1483
QY 1263 CTACGCTACGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGGAGG 1322
Db 1484 ATAGGCGCGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGGAGG 1543
QY 1323 CGTACCGGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGGAGG 1382
Db 1544 CGACCGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGGAGTGGGAGG 1603
QY 1383 CGCGCTGCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGTGGTGGGCGCGCTTTCGCG 1442
Db 1604 GATCGAGGCGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGTGGGAGGAG 1663
QY 1443 GATGGTGGCAACTGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGTGGGAG 1502
Db 1664 TCTCCAGGCGCGCTTTCGCGCGCTTTCGCGCGCGCTTTCGAGGAGGAGTGGGAGG 1723
QY 1503 GGGCGCTTTCGCGCGCTTTCGCGCGCTTTCGAGGAGGAGTGGTGGTGGTGGTGGTGG 1527
Db 1724 GGAGCTGCTTTCGCGCGCTTTCGCGCGCTTTCGAGGAGGAGTGGTGGTGGTGGTGG 1748

RESULT 13
US-08-941-445A-8
; Sequence 8, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303

MOLECULE TYPE: CDNA

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2003, 21:49:59 ; Search time 177.291 Seconds
(without alignments)
15416.986 Million cell updates/sec

Title: US-09-980-771A-4

Perfect score: 1953

Sequence: 1 gcgtgacatcgatggt.....ccgccaccgcgaatccgcgc 1953

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475.8	24.4	2267	9	US-09-961-077-25
2	314.6	16.1	2399	9	US-10-138-075-1
3	275.2	14.1	2179	9	US-10-138-075-3
4	218.2	11.2	2825	10	US-09-952-677-5
5	118.2	6.1	2239	10	US-09-952-677-1
6	102	5.2	2712	10	US-09-748-033-4
7	94.2	4.8	790	10	US-09-966-881-44
8	86.6	4.4	1266	9	US-10-145-415-98
9	84.2	4.3	2307	9	US-09-893-519A-87
10	83.2	4.3	1427	10	US-09-974-300-757
11	82.2	4.2	805	10	US-09-966-881-43
C 12	81	4.1	12441	9	US-09-988-384B-3
C 13	81	4.1	13613	9	US-09-860-846-3
C 14	81	4.1	13613	9	US-09-836-821-3
C 15	81	4.1	13613	10	US-09-861-289-3
C 16	76.4	3.9	813	10	US-09-966-881-45
C 17	76	3.9	1318	9	US-09-934-900-15
C 18	75.4	3.9	446	10	US-09-864-761-20699
19	75.2	3.9	1896	9	US-10-124-880-15

20	74.8	3.8	1407	10	US-09-815-242-4089	Sequence 4089, Ap
21	74.8	3.8	15872	9	US-09-860-846-1	Sequence 1, Appli
22	74.8	3.8	15872	9	US-09-988-384B-1	Sequence 1, Appli
23	74.8	3.8	15872	9	US-09-836-821-1	Sequence 1, Appli
24	74.8	3.8	15872	10	US-09-861-289-1	Sequence 1, Appli
25	74.6	3.8	1266	9	US-10-145-415-104	Sequence 104, App
26	74.2	3.8	1770	9	US-10-100-957A-1	Sequence 1, Appli
27	73.6	3.8	8421	9	US-09-976-059-1	Sequence 1, Appli
28	72.4	3.7	3468	9	US-09-988-462-2	Sequence 2, Appli
29	72.2	3.7	299	10	US-09-294-093B-3520	Sequence 3520, Ap
30	72.2	3.7	824	10	US-09-894-633A-83	Sequence 83, Appli
31	71.4	3.7	3624	9	US-09-988-462-6	Sequence 6, Appli
C 32	71.4	3.7	12733	9	US-10-032-393-47	Sequence 47, Appli
C 33	71.4	3.7	12733	9	US-10-032-393-8	Sequence 8, Appli
34	71.2	3.6	1182	9	US-09-364-847-1	Sequence 1, Appli
35	71.2	3.6	1926	9	US-09-364-847-9	Sequence 9, Appli
36	71.2	3.6	1926	9	US-09-364-847-18	Sequence 18, Appli
37	70.8	3.6	1415	9	US-09-934-900-11	Sequence 11, Appli
38	70.6	3.6	1635	10	US-09-864-761-20241	Sequence 20241, A
39	70.6	3.6	1973	10	US-09-864-761-3471	Sequence 3471, Ap
C 40	69.8	3.6	1075	10	US-09-864-761-19241	Sequence 19241, A
C 41	69.8	3.6	1403	10	US-09-864-761-2513	Sequence 2513, Ap
42	69.8	3.6	2010	12	US-10-032-717-9	Sequence 9, Appli
43	69.8	3.6	4689	9	US-09-860-846-34	Sequence 34, Appli
44	69.8	3.6	4689	9	US-09-988-384B-34	Sequence 34, Appli
45	69.8	3.6	4689	9	US-09-836-821-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1

US-09-961-077-25
; Sequence 25, Application US/09961077
; Publication No. US20030014775A1

GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS

NUMBER OF SEQUENCES: 1263

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/961,077

FILING DATE: 21-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/679,645

FILING DATE: July 12, 1996

APPLICATION NUMBER: 60/001,135

FILING DATE: July 13, 1995

APPLICATION NUMBER: 08/300,726

; TYPE: DNA
; ORGANISM: Glycine max
US-10-138-075-3

Query Match 14.18; Score 275.2; DB 9; Length 2179;
Best Local Similarity 52.78; Pred. No. 1.6e-53;
Matches 820; Conservative 0; Mismatches 628; Indels 108; Gaps 6;
QY 11 TCGTATGTTGCTGCTGAGTTCGGCCCTGCTCCAGACGGCGGCTGGGCGATGTA 70
DB 323 TCATAATATAGAACCGAGGTGCTCCATGTCGAACACTGGTGGGTGGAGATGTC 382
QY 71 CTGTGGCTGCTTATGAGTGTCAAGCGCGCCACCGGCTGATGACCAATTCGCCCTC 130
DB 383 TTGGAGGTCTACCAACCGCATTTGGCAGGTTCGATGATGATGATGATGATGATG 442
QY 131 GCTAGGACAGTACGCTGAGCTGGGACCTCGTGTGCTGGACATCATGG----- 184
DB 443 GCTATGACCACTACAAAGATGATGGGATACAAAGTGTGTAATGAGGTGAAGTAGAG 502
QY 185 -----GGGAGAAGGTCCGCTACTTCCACTCCATCAAGAAGGCGTGCACCGCTGGA 238
DB 503 ATAGAACAGAAAGGTTCGCTTCTTCCATGTTATAGAGGGAGTGTGATCGTGTG 562
QY 239 TTGACCAACCTGTTCTGCGCAAGTCTGGGCAAGACCGGCTCCAGCTGTACGGCC 298
DB 563 TGGATCACCTTGTGTTCTTGAAGAGGTATGGGGGAAACTGGACAAAACCTTTATGGAC 622
QY 299 CCGCTCGGCGCTGACTACCTGAGCAACCAAGCGCTTCGCCCTGTCTCAAGCGCG 358
DB 623 CAATCTAGGAATGATTACGAAGACAACTGCGTGTGAGCTTTAGCCCTCTTTGCCAGGCTG 682
QY 359 CTATTGAGGCTCCGCGCTGCTGCTGCTGCGCC-----G 394
DB 683 CTTTGAAGCCCAAGGTTCTGAGCTTAATTCAGTAATATTTCTGCAACCATATG 742
QY 395 GCGAGAGCTGCTGCTGCTGCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 454
DB 743 GTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 802
QY 455 AGGACAGTACCAAGGCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 514
DB 803 AAGTATGTACCAAGTCAAGGCGCTATACGAATGCGCGGTTGTTTGTATATCCACA 862
QY 515 ACATGCTCTCCAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
DB 863 ACATGCTCTACCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922
QY 575 CCGCTCTTACCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
DB 923 AATTAGAGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 958
QY 635 CCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 694
DB 959 -----TTAAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 991
QY 695 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 754
DB 992 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
QY 755 AGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
DB 1052 AACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
QY 812 -----GCATTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
DB 1112 AIGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1171
QY 863 CCGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922
DB 1172 CTGACAAATATATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1231
QY 923 CCAAGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 982

DB 1232 TGAAGAAGCCCTCCAGACAGAGTGGATTCAGTCCAGACAGAAATATTCCTCTCATG 1291
QY 983 CTTTCATGCGCCCTGGAGGAGCAAGAGGTGTGGACATATCTGCGCCGCTGCGCA 1042
DB 1292 GTTTCATGTTAGGCTTGAAGAGCAAAAGGTTCTGATATCTTGCAGAGGCTATCCCC 1351
QY 1043 AGATCCTGCGCCACCCCAAGGTGAGATCGCCATCTCTGGTACCGCAGGCGGCTAG 1102
DB 1352 AATTAT---CAAGAGAAATGTTCAAGTGGTGGTACCCCTAGGAACAGAAAAAACAATGG 1408
QY 1103 AGAAGCTGTGAACCCATCGCCGCAACAGTACAAAGGCGCGCCCAAGGCGTGGTCAAGT 1162
DB 1409 AAACGACGCTTGAAGAACTTGAATATCAATCCCTGATAAGCCAGAGGAGTGGCAAAAT 1468
QY 1163 TCTGCGCGCCCTGGCGCACATGCTACCCGCGGCGCCGCTCATGCTGCTGCTGCTGCTG 1222
DB 1469 TCAATGTTCCCTAGCCACATGATAATAGCTGGAGCTGATTTATATTTGTTCTPAGCA 1528
QY 1223 GCTTCGAGCCCTGCGGCTGATCCAGCTGACGCCATGACATGCTGCTGCTGCTGCTGCTG 1282
DB 1529 GATTGAGCCTTGTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1588
QY 1283 TAGCCTCCACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1342
DB 1589 TTGCTCAACAGGTGATGTTGACACTGTCAAGAGGCTTCACTGGATTTGATGCTGCTG 1648
QY 1343 GCGCCCTGA-----ACCCGACAGCTGACGAGCTGACGCCGCGCTGCTGCTGCTGCTG 1396
DB 1649 GTGCTTCAATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1708
QY 1397 CGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1456
DB 1709 CTGTCAAAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1768
QY 1457 GCATCAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1512
DB 1769 GCATGCTCAAGATCTTCAAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1824

RESULT 4

US-09-952-677-5
; Sequence 5, Application US/09952677
; Patent No. US20020138876A1

GENERAL INFORMATION:

APPLICANT: Block, Martina
Lorz, Horst
Luticke, Stephanie
Walter, Lennart
Frohberg, Claus
Kossmann, Jens

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
FROM WHEAT WHICH ARE INVOLVED IN STARCH
SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., C/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952.677

FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/196,390

FILING DATE: 19-No. US20020138876A1-1998

Query Match	11.2%	Score 218.2	DB 10	Length 2825	
Best Local Similarity	50.1%	Pred. No. 1.3e-40			
Matches 769	Conservative	0	Mismatches 688	Indels 78	Gaps 6
QY	5	TGACATCGTGATGGTTGCTGCTGAGTTCGCCCTTGGTCCAAAGCGGGCGGCTCGGGCG	64		
Db	1084	TGAACGTGGTCGTCGGCTGCTGAGTGTCTCCCTGGTCAAAACAGGTGGTCTGGGAG	1143		
QY	65	ATGTGACTGTGGCCCTGCCTATTGAGCTGCTGAAGCGCGCCACCGCGGTCATACACATTG	124		
Db	1144	ATGTTGGGGTGTCTGCCCCAAGCTTTGCCAAAGAGAGACATCGTGTATTGTTGTGG	1203		
QY	125	CCCTCGCTACGACCAAGTACGCTAGCGCTGGGACACCTCGGTGGTCTGGACATCATGG	184		
Db	1204	TACCAAGGTATGGGGACTATGAAGAAGCTACGATGTCGGAGTCCGAAAATATCAAGG	1263		
QY	185	GGGAGAGGTCCGTACTTCCACTCCATCAAGNAGGCGTGCAACCGCGTGTGGATTGACC	244		
Db	1264	CTG-----CTGGACAGGATATGAAGTGAATATTTCATGCTTATATCGA	1309		
QY	245	ACCCTGTGTTCTGGCCAAAGGCTGGGGCAAGACCGGCTCCAGCTGTACGGCCCCCGCT	304		
Db	1310	TGGAGTGTATTTGTGTTGTTGATTCAGCGCTCCTCTCTCCGAC-ACCCTCAGGAAGACATTT	1368		
QY	305	CCGGCGCTGACTACCTGGACACCAAGCGCTTCGCCCTGTTCGCAAGCGCGCTATTG	364		
Db	1369	ATGGGGGCAGCAGACAGGAATATCAGCGCATGATTTGTCTGCAAGGCGCGTGTG	1428		
QY	365	AGGCTGCCCGCGTGTGCCCTTGGCCCGCGGAGGACTGCG-----TCTTCG	412		
Db	1429	AGGTTCCATGGCACGTTCCATCGGCGGTGTCCTTATGGGATGGAATCTGGTGTATA	1488		
QY	413	TGGCCAAAGACTGGCACTCCGCCCTGGTGGCCGTCCTGCTGAAGACAGTACCAACCCA	472		
Db	1489	TTGAAATGATTGGCACAGCGACCTCGCTGTCTATCTGAAGCATATTACAGGGACC	1548		
QY	473	AGGGCCAGTTACCAAGGCCAAGTCGGTCTGGCTATCCAAACATCGCCTTCCAGGGCC	532		

746	ACGCGACCCAGATC---GCTGCGCATGCGCGCGGTGTGAGCTGGACACCGTATCC	802
QY		
Db		
883	ATTTCATGGAGGTCACAACCTGCTGAAGGTGGACAGGCGCTCAATGAGCTTTAAGCTCC	942
QY		
Db		
803	GGCCCAAGGCGCATTTAGGCGCATTTGAAACGGCATGGACATTTGAGGACTGGAACCCCAAGA	862
QY		
Db		
943	GA AAAAGTGTATGTAATGAATTTGTAATTTGGAATTTGACATTTAATGATTTGAACCCCAACA	1002
QY		
Db		
863	CGACAAAGTTCTCTGCTCGCGCCTACGACCAACAAGCGCTTACGCGCGCAAGCGCGCGG	922
QY		
Db		
1003	CAGACAAAGTGTCTCCCTCATCATTTCTGTGATGAOCTCT--CTGGAAAGGCCAAAT	1059
QY		
Db		
923	CCAAGAGGCGCCTGCRAGGCGGAGCTGGGCGTGGCTGTGACCCACCGCCCTCTTTGG	982
QY		
Db		
1060	GTAAGCTCAATTTGCAAGAGGAGTTGGGTTTACCTGTAAAGGAGGATGTTCTCTGATTG	1119
QY		
Db		
983	CTTTCATCGGCCCTTGGAGGACGAGAAGGTTGTGGACATCATCTTGGCGCGCTGCCCA	1042
QY		
Db		
1120	GC TTTATTTGGAACATGGATTTACCAAGAGGCAATTGATCTCATTAANTGGCCATTCAG	1179
QY		
Db		
1043	AGATCTCTGGCCACCCCAAGTGCAGATGCCATPCCTCGGTACGGCAAGGCGCGCTACG	1102
QY		
Db		
1180	AGCTCATG---AGGAGGACGTGCAATTTGTCATGCTTGGATCTGGGATPCCAATTTTG	1236
QY		
Db		
1103	AGAAGCTGTGTAACGCATCGGACCAACGATACAAAGGCCCGCGCAAGGGCGTGTCAAGT	1162
QY		
Db		
1237	AAGGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAATTCGTGGATGGTTGGAT	1296
QY		
Db		
1163	TC TCGGCGCCCTGGCGGCACATGCTCACCGCGCGCGCGACTTCATGCTGGTGCCTCGC	1222
QY		
Db		
1297	TTAGTGTTCAGTTTCCACAGATAACTGCAGTTGCGATATATTGTTAATGCCATCGA	1356
QY		
Db		
1223	GCTTCGAGCCTCGGGCCTGATCAGCTGCACGCCATGCACCTACGCTACCGTGCCTGG	1282
QY		
Db		
1357	GATTTGAACCTTGGCGTCTTAATCAGCTATATGCTATGCAATATGTCATGTCACAGTTTCTCTGAT	1416
QY		
Db		
1283	TAGCTCCACCGGCGGCTGGTCGACACCGTCAAG	1317
QY		
Db		
1417	TTCATGAACTGGGGGCGCTCCGAGACACAGTCGAG	1451
QY		
Db		
RESULT 6		
US-09-748-033-4		
; Sequence 4, Application US/09748033		
; Patent No. US2002069431A1		
; GENERAL INFORMATION:		
; APPLICANT: Broadway, Roxanne M.		
; APPLICANT: Gongora, Carmen A.		
; TITLE OF INVENTION: EFFECT OF ENDOCHITINASE AND CHITOBIOCIDASE AND THEIR		
; TITLE OF INVENTION: ENCODING GENES ON PLANT GROWTH AND DEVELOPMENT		
; FILE REFERENCE: 19603/3091		
; CURRENT APPLICATION NUMBER: US/09748,033		
; CURRENT FILING DATE: 2000-12-22		
; PRIOR APPLICATION NUMBER: 60/172,003		
; PRIOR FILING DATE: 1999-12-23		
; NUMBER OF SEQ ID NOS: 8		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 4		
; LENGTH: 2712		
; TYPE: DNA		
; ORGANISM: Streptomyces albidoflavus		
US-09-748-033-4		
Query Match 5.2%; Score 102; DB 10; Length 2712;		
Best Local Similarity 43.8%; Pred.No. 2.7e-14;		
Matches 597; Conservative 0; Mismatches 755; Indels 12; Gaps 3		
QY	569	CCGAGCGCGCCTTTTACAAAGCTTCTCGGACGGCTATCCCAAGGTTTACACTGAGG 628
Db	915	CCGAGCGCGCGAGCGCGCGCGCCGACCGCTCTCTACACAGGACGCGAGGACTGGG 974
QY	629	CCACCCCATGGAGGACGAGACCGCCCGCTGACGGGAAGACCTACAGAAGATCA 688

Db 975 GCAGCGGCTTCGAGGCAAGTGAGCGGTGAAGACACCGGACCGCCCGCCCTCAGGGCT 1034
QY 689 ACTGGCTGAGGGTGGGATTAATCGCGCGGACAGAGCTGGTGAATGTGTCGCCCACTACG 748
Db 1035 GGACCTCTGGAGTGGGACTTCCCGCGGAAACAGGTGACCTCGGCTGGGACGCCGACG 1094
QY 749 CGACCGAGATCGCTGCGGATGCGCGCGCGGTGTGGAGCTGGACACCGTCAATCGCGCCA 808
Db 1095 TCACCAACAGCGGACCACTGGACCGCCCAAGAAAGAGCTGGCGGGGAGCTCGGCC 1154
QY 809 AGGCATTTAGGGCAITTTGAACGGCATGGACATGAGGAGTGAACCCCAAGACCGACA 868
Db 1155 CCGGCGCTCGGTGAGCTTCAACGGCAGCCCGCGGACCCCTCGGGGTGCA 1214
QY 869 AGTTCCTGTCTGCGCCCTAGACCAAGACAGCGGTCTACGCGGCGGAGCGCCGCCAAGG 928
Db 1215 AGCTCAACGGCGCTCTCTGGGAGCGGCGGCGGAGCTCCCGCGGACACCCCGCCACCGCC 1274
QY 929 AGGCTCTGACGGCGGAGCTGGGCTGCTGTGGACCG--CACCAGCCCTGTTCGCT 985
Db 1275 CCGGACCCCGGACGCTGAGCTTCAACGAAGACTCGGTGAAGCTCTCTGGAAGCGG 1334
QY 986 TCATCGCCCTCGGAGGACAGAGGGTGTGGACATCATCTGGCGCGCTGCCAAGA 1045
Db 1335 CCACCGACGACAGGGCGTCAAGAACTACGACGTCTCTGCGGAGCGGCGCAAGTCCCA 1394
QY 1046 TCTGCGCACCCCAAGGTGCATCGCATCTCTGGGTACCGGACGAGCGGCTACGAGA 1105
Db 1395 CCGTACCGCCACCACTTACCGACGACAGAACTCGCCCGCGGACGACTACTCTACT 1454
QY 1106 AGTGTGTAACGCATCGGCACCAAGTACAAGGCGCGGCAAGGGCTGTCAAGTTCT 1165
Db 1455 CGGTCCAGCGCGACACCGCGACGACGCGCGCGGCTACGCGCCCGGTCAAGGTCA 1514
QY 1166 CGGCGCCCTCGGCGACATCTCACCGCGCGCGGCTCATCTGCTGGTCCCTCGCGCT 1225
Db 1515 CCACCGCGCGGACGCGCGGCGCGCGCGCGCGCGGAGAT-----CAACC 1568
QY 1226 TGGAGCGCTGCGGCTGATCCAGCTGACGCGGCGGCTGACGTGCTGCTGCTGCTGCTG 1285
Db 1569 TCGGTACTTACCGAGTGGGCGTCTACGGCGCACTACCACTCAAAACCTGTGA 1628
QY 1286 CTTCCACCGCGCGCTGTGTCGACACCGTCAAGGAGGCGGTACCGGCTTCCATCGGCG 1345
Db 1629 CTTGCGGCTCGCGGAGAGATCACCACTCACTACTCTTGGGCAACGTCACGCGCG 1688
QY 1346 CCTGAACCCCGACAGCTGGAGGCTGACGCCAGCCCTGGCGCGGACCGTGGCGG 1405
Db 1689 GC---AAGTGCACCATCGGTGACAGCTTCGCGGCTACGACAGGGGTACCGCGCGG 1745
QY 1406 GTGCCAGCGAGGTGTTGGGCGGCGGCTACCGGAGATGTGGCCAACTGATCAGCG 1465
Db 1746 AGTCGGTGCAGCGGCTCGCGGACACTTGGGACGAGCGCTGCGCGCAACTTCAACGAG 1805
QY 1466 AGGACTGTCTCTGTTCCAGCGCGCGGCAAGAGTGGAGGCGCTGCTGGAGGAGTGTGT 1525
Db 1806 TCCGCAAGTCAAGCCCAAGTACCGGCACATCAAGTCTCTGCTTTCGGCGGCTGA 1865
QY 1526 AGGCAAGGGGCGGTGGCCACCGCCAAAGAGAGGAGATCAAGTGGCCGCTGGCGGAG 1585
Db 1866 CTTGTCGCGGCGGCTTACCGAGCGCGTGAAGAACCCCGCGGCTTCGCAAGTCTGCG 1925
QY 1586 AGATCCCGGCGACCTCGCGCGCTGTCTAGCCCCCAACACTGAAAGCCGCTGTCG 1645
Db 1926 AGGACTGTGTGAGGACCGCGGCTGGGCGGAGCTTTCGACGGCATCGACCTCGACTGG 1985
QY 1646 CTTGCGTGGAGGCAACCGCGCGCGCGCCCAAGGTGCGGACCAACCGCCCGCCATGG 1705
Db 1986 AGTACCCGAGCCCTGCGGCTTACCTGAGCAGCTCGGTCGCGGCTCGGCTGGAAGACA 2045
QY 1706 GGGCTGGCGGCGACCAACCCCTCGGCGCGCTCGCGCGCGGCGGCGGCGGCTGGA 1765

Db 2046 TGGTCCAGCGATGCGCGCGCCAGTTCCGACCGACCTGCTACCGCCGCCATCACCGCG 2105
QY 1766 CCACCTAAGCGCGCGCTGCGCGCCACCGCCACCGCCCAAGACCGCTGCGCTCAAGCTGG 1825
Db 2106 AGCCAGCTCGGCGGCAAGCTCGACGCGCGGAGTACGCGGCGCGCGCCAGTACTTCG 2165
QY 1826 CCGTGTAGGCTTCCACCACTCGACCTCGGAGAAAGCGGCTGCTTCCCAAGCGCAACGCA 1885
Db 2166 ACTGTACAACGTGATGACTACGACTTCTTCGGGCGCTGGACAGACCGCGCGCGCG 2225
QY 1886 ACGTGTCTCGGCTTCCAAAGACCTCGGCTGCGGCTGCAAGCGCCCTGTC 1929
Db 2226 CGCCCCACTCGGCGCTGAACCTCTACAGCGGATCCCGCAAGGCC 2269

RESULT 7

US-09-966-881-44
; Sequence 44, Application US/09966881
; Patent No. US20020120960A1
; GENERAL INFORMATION:
; APPLICANT: Seymour, Graham
; Bird, Colin
; Medina-Suarez, Rosybel
; TITLE OF INVENTION: Genetic control Of Fruit Ripening
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca Ag Products Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,881
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/242,860
; FILING DATE: 29-Mar-1999
; APPLICATION NUMBER: GB 9618862.8
; FILING DATE: 10-SEP-1996
; APPLICATION NUMBER: GB 9708366.1
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: PCT/GB97/02424
; FILING DATE: 08-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: SEE 50183/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 790 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: U-D111
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-966-881-44

Query Match

Best Local Similarity 4.8%; Score 94.2; DB 10; Length 790;
Matches 210; Conservative 57.2%; Pred. No. 1.7e-12;

Mismatches 144; Indels 13; Gaps 2;

QY 1 GCGCTGGACATCGTGATGTTGCTGCTGAGTTCGCGCCCTTGGTCCAAAGACGCGGCGCTG 60

[illegible]

Query Match	4.3%;	Score 83.2;	DB 10;	Length 1427;
Best local Similarity	47.7%;	Pred. No. 5e-10;		
Matches 309;	Conservative 0;	Mismatches 333;	Indels 6;	Gaps 2;
QY	671	AGACCTACAAGAAGATCAACTGGCTGAAGGGTGGCATATACGCCCGCAACAGCTGGTGA	730	
Db	578	AGITTTATGGGAACATTAAATTATGSAAGCGGCAATTATCCCGCTGATCAGGTGACAA	637	
QY	731	CTGTGTGCGCCAACTACGGCAACGGAGATC---GCTGCCGATCCGCCCGCGGTGTGGAGC	787	
Db	638	CGGTCACTCGGAGCTACCGCGATGAAATCTTGACTCCATCTACGGCAGCGGCTTGAAG	697	
QY	788	TGGACACCGGTCACTCCGCCCAAGGGCATTTGAGGGCATTTGSAOCCGCATGACATTGAGG	847	
Db	698	GGGTGTGTGACACAGAAGGATGCACTACAGAGCAATTTAAACGGGATTGACGATGTGC	757	
QY	848	AGTGGAAACCCAAAGACCGACAGTTCTGTGTGCCCTTACGACCAGAACAGCGCTCTACG	907	
Db	758	TGTACAGACCTTTAAACGATCCGCACTGCATCTATCATTAAG---ATGCCGTCAACCGGG	814	
QY	908	CCGGCAAGCGCGCGCAAGGAGGCCCTGCAAGCGCGAGCTGGCCCTGCCTGTGACACCCA	967	
Db	815	ACGGAACCGGAATAAAGCCGTGATCCAGAGACATTCGGTGTCCGGTGAATGAAG	874	
QY	968	CGCGCCCTCTGTTCGCTTCACTCGGCCCGCCTTGGAGGACAGAAGGGTGTGACATCATCC	1027	
Db	875	ACATTCGCGTCACTAGCATGTGTGGCAAGGCTGACGAACCAAAAGGCTTCGATTTGATCA	934	
QY	1028	TGSCGCGCCTGCCCAAGATCTCTGGCCACCCCAAGGTGCAGTCCCATCTCGGTACCG	1087	
Db	935	ACGGGTATTGATGACTGTTTGAAGAAGAAGACATGCAGTCACTGTTTGAAGAACC	994	

QY	1088	GC	AAGCGCGCCTACGAGAAAGCTGGTGAACGCCATCCGACCAAGTACAGAGGCGCGGCCA	1147
Db	995	GACA	AGCGGAATTTGAAATTTACTTCCGTATATGGAGCATGCTTTTCCGGACAGGTGCA	1054
QY	1148	AGGG	CGTGGTCAAGTTCTCGGCGCCCTCGGCGCACATGTCACCGCGCGCGCGCACTTCA	1207
Db	1055	AGCG	CGTATATCGGTTTTCATGAACCGCTACGCGCAAGATTATGCGCGGAGCGATCTTT	1114
QY	1208	TGCT	GTGTGCCCTCGCGCTTCGAGCCCTCGCGGCTGATCCAGCTGCACGGCCATGCATCAGG	1267
Db	1115	TCT	GATGCCCTTCAAAATTCAGCGGTGCGGTCTTGGACAGCTGATTGCCCTCAGGTACG	1174
QY	1268	GTAC	CGTGGCCCGTGGTAGCCTCCACCGCGGCGCTGTGCGACACCGTCA	1315
Db	1175	GCG	GGTGGCGGTTGTTCAGGAAACAGGCGGGCTTCATGATACGGTGA	1222

```

RESULT 11
US-09-966-881-43
; Sequence 43, Application US/09966881
; Patent NO. US20020120960A1
; GENERAL INFORMATION:
; APPLICANT: Seymour, Graham
; Bird, Colin
; Medina-Suarez, Rosybel
; TITLE OF INVENTION: Genetic Control Of Fruit Ripening

```

Query Match 4.2%; Score 82.2; DB 10; Length 805;
Best Local Similarity 57.8%; Pred. No. 8.6e-10;

```

Matches 170; Conservative 0; Mismatches 111; Indels 13; Gaps 1;

QY      1  GCGCTGGACATCGTGATGTTGCTGCTGAGGTCCGCCCTTGGTCCAAGACGGCGGCGCTG 60
Db      1  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY     310  GGGATGAACATAGTCTTTGTGCGGCGCTGAGATGGCTCCCTGGANTAAACCCGGAGGACTC 369
Db     310  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY     61  GCGCATGTGACTGTGTGGCTCGCTTATGAGTCAAGCGCGGCCACCCGCTCATGACC 120
Db     61  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY     370  GGTGATGTTCTTGGAGGACTGCCACGGCCCATGGCTGCAAAATGGACACACAGTGTGACT 429
Db     370  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    121  ATTGCCCTCGTAGCACACGACTACCTGACGCCGCGGACACCTCGGTGGTGTGCG----- 172
Db    121  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    430  ATAGCTCCACCGTATGATGATCAAGGATGGTGGGATACAAATGTCTTGGCTGANTTA 489
Db    430  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    173  -----TGGACATCATGGCGAGAGGTCCGCTACTTCCACTCCATCAAGAGGCGGTGCA 227
Db    173  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    490  AAANTTGGAAATGAATTTGAAAGANTCCGCTTCTCCACTGCTATAAANAAGAAATTGA 549
Db    490  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    228  CGCGCTGTGGATGACACCCCTCGTTCCTCGGCCAAAGTCTGGGGCGAAGACCGG 281
Db    228  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY    550  CAGGGTTTCAATGTATCATCTCTTTGTTCTTGA AAAAGTGTGGGGA AAAA ACTGG 603
Db    550  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-09-988-384B-3/c
; Sequence 3, Application US/09988384B
; Publication No. US20030073824A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.536US1
; CURRENT APPLICATION NUMBER: US/09/988,384B
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/US99/14398
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 53
; SEQ ID NO 3
; LENGTH: 12441
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-988-384B-3

```

QY 1037 TGCCCAAGATCCTGGCCACCCCAAGGTGCAGATGCGCCATCCIGGGTACCGCCAGGGCCG 1038

Db 11361 ACCTCCCGCGCTCTCTGTCGCGGACCAACGACGCGCTCAACACACCAAGTACG 11302
QY 1097 CCTACGAGAAGCTGGTCAACCGCATCGGACCAAGTACAAGGCGCGGCCAAGGCGGTGG 1156
Db 11301 TGATCTCGATTCGAGAGGCGCCACCAACCGGATCCACCGGACCTCTGTATGAGTCC 11242
QY 1157 TCAAGTTCGSGCGCCCTGGCGCATATGCTCAACGCGCGCGCGGCTTCAATGCTGTGC 1216
Db 11241 TGAAGGCGGAAGCGTGCACACCGCGCTTCTCTCGCGGCTGCCAGAGCTGGAGC 11182
QY 1217 CTTGCGGCTTCGAGCGCTCGGCGCTGATCCAGCTGACGCGCATGCACTACGTTACGTCG 1276
Db 11181 CGTACCGCGGCGACGCGACGCGCGCTGCGGACACCGAACGCTCGCGCGCGGTGC 11122
QY 1277 CGTGTAGCTCTCACCGCGCGCTGTGTCACACCGCTCAAGAGGCGGTCAACGCGTTC 1336
Db 11121 TGTCCCTCGGACCGGACCGCATCGGCGACGACGACATCCCGCGGTGCGCGACCTGC 11062
QY 1337 ACATGGCGCCCTGAACCCCGACAAAGCTGGACGAGCTGACGCGGACGCGCTCGCGGCA 1396
Db 11061 TGGCTCTCTGCGGACCGCGCGGCGAACTGACCGGCGGCGACCGGACCGCGCGCG 11002
QY 1397 CGTGGCGGCTGCGACGAGGTGTTGCGGCGGCGCGCTACCGCGGAGTGGTGGCAACT 1456
Db 11001 CCGCGCTCGGCG 10952
QY 1457 GCATCAGCGAGGACCTGCTGTGTCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1516
Db 10951 TGACG 10892
QY 1517 AGTGGTGTACGCGCAAGGCGCGGTGGCGACCGCGCGCGCGCGCGCGCGCGCGCGCG 1576
Db 10891 ATCTGGGCGCGCGGTCCACGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10832
QY 1577 TTGCGGAGAGATCCCG 1636
Db 10831 CCGAGCG 10772
QY 1637 CCGTGTGCGCGCTCGTGGAGGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1696
Db 10771 GCCCTTACCGCGGTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10712
QY 1697 CGCGCATGGCGCGGTGGCG 1756
Db 10711 GCGCGCTCTCGCGCGGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10652
QY 1757 CCAAGGTGACCACTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1816
Db 10651 CG 10592
QY 1817 TCAAGTGGCGGTGAGCGCTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1876
Db 10591 CGCGCTCGCGAGGAGCGCGGTCTTCCGCTACAGCGTGGCGCTTACCGCGCGCGCGCG 10532
QY 1877 GCA 1879
Db 10531 GCA 10529

RESULT 13

US-09-860-846-3/c
; Sequence 3, Application US/09860846
; Patent No. US2002016742A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D. H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/860.846
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537

; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 13613
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-860-846-3

Query Match

4.1% Score 81; DB 9; Length 13613;
Best Local Similarity 42.7%; Pred. No. 1.5e-09;
Matches 488; Conservative 0; Mismatches 645; Indels 10; Gaps 1;

QY 737 CGCCCAACTACGCGACCGAGATCGCTGCCATGCGCGCGGTGTGAGTGTGACACCG 796
Db 12348 CGTTCGAGCG 12289
QY 797 TCATCCGCGCAAGGGCATTTGAGGCAATTTGAAACGGCATGGACATTTAGAGAGTGAACC 856
Db 12288 CCAAGCGCGTCAACGCGCTTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12229
QY 857 CCAAGACCGGACAAAGTTCTCTGTCGCGCGCTAGCAGCAGACAGCGCTTACGCGCGAAG 916
Db 12228 CCGGATCGCGCGCTCCACACTTCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 12169
QY 917 CCGCGCGCAAGGAGCGCGCTGAGCGCGAGCTGGCGCTTGCCTGTGACCGCGCGCGCGCG 976
Db 12168 GGACCAACGCAAGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12109
QY 977 TGTTCGCTTCATCGCGCGCGCTGGAGAGCAGAGGCTGTGACATCATCTTGGCGCGCGCG 1036
Db 12108 TTCCCGAGGTTCATCGACCGGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12049
QY 1037 TGCCCAAGATCTTGGCG 1096
Db 12048 ACTCCCGCGGTCTCTGTCG 11989
QY 1097 CCTACGAGAGCTGTGTAACCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1156
Db 11988 TGATCTCGAGATCGAGGCG 11929
QY 1157 TCAAGTTCG 1216
Db 11928 TGAAGCGCGAGCGCGTGCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11869
QY 1217 CCGCGCGCTTCGAGCG 1276
Db 11868 CGTACCG 11809
QY 1277 CCGTGTAGCTTCCACCG 1336
Db 11808 TGTCTCTCG 11749
QY 1337 ACATGGGCGCGCTGAACCG 1396
Db 11748 TCGCTCTCTGCG 11689
QY 1397 CCGTGTGCG 1456
Db 11688 CCGCGCTCG 11639
QY 1457 GCATCAGCG 1516
Db 11638 TGACCG 11579
QY 1517 AGTGGTGTACGCGAAGGCG 1576
Db 11578 ATCTGGGCG 11519
QY 1577 TTGCGGAGAGATCCCG 1636
Db 11518 CCGAGCG 11459

QY	1637	CCGTGTCGGCGCTCGGTGAGGGCAACGGCGCCGCCCAAGTCTGGCACCACGGCCC	1696
Db	11458	GCOCCTTCAACCCGCTGAGAGAGCGCCGCCAACGACTGGGCGTTCAGCCGGGACGCTTCC	11399
QY	1697	CCGCATGGGGCGGTGGCGGCGGACCAACCCCTCGGGGCCCTCGCGCCGCGCGCGCACCC	1756
Db	11398	GGCGCCTTCCTCGCCCTGTTCGGGAGTGTCCTCGGAGCTCGCACCGCGGTCTGAGACCGGCC	11339
QY	1757	CCAAGGTGACCACTACAAGCCCGCCCTTCGCCGCCACCGCCAAAGACCCAGACCGTGGCC	1816
Db	11338	CGCGCGGGGCGTACTTGAAGAACAACCCCTGCTCCCGCTCGAACAGCGGGCGTCTTCGACG	11279
QY	1817	TCAAGCTGGCGGTGAGCCTTCACCACTCGACCTCGAGAACGGCGCTGCTCCCAAG	1876
Db	11278	CGCGCTCGCCAGGAAGCCCTCTTCCGTTACAGCTCGGCCCTACCCCCGCCGACCT	11219
QY	1877	GCA	1879
Db	11218	GCA	11216

```

RESULT 14
US-09-836-821-3/c
; Sequence 3, Application US/09836821
; Publication No. US20030087405A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438U.SI
; CURRENT APPLICATION NUMBER: US/09/836, 821
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 13613
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-836-821-3

```

Query Match	4.1%;	Score 81;	DB 9;	Length 13613;
Best Local Similarity	42.7%;	Pred. No. 1.5e-09;		
Matches 488;	Conservative	0;	Mismatches 645;	Indels 10; Gaps 1;
QY	737	CGCCCAACTACGCGACCGAGATCGCTGCGCGATGCCGATCCGCGCGGTGTGGAGCTGGACACCG	796	
Db	12348	CGGTGCGAGCGCGCGCGCGGAGCCTCGGCGACGCGGAGGTCTTCAGCTTCACGCCCA	12289	
QY	797	TCATCGCGCCCAAGGGCATTGAGGGCAATTGTGAACGCGCATGGACATTTAGAGATGGGAAC	856	
Db	12288	CCAAGGCGCTCAACGCGCTTCGAGGGGGGCGCGCTGCTACCGCAGACGCGACCTCGCG	12229	
QY	857	CCAAGACCGACAAGTTCCTGTCTGCGCCCTACACACAGACACAGGCTACGCCGCGAAG	916	
Db	12228	CCGGATCCGCGCCCTCCCAACTTCGGGTTTCGACCTGCCGCGGAGCGCCCGCGCGCG	12169	
QY	917	CGCGCGCCCAAGGAGGCCCTTCAGGCGCGAGCTGGCGCTGCGTGTGGACCCACCGCCGCC	976	
Db	12168	GGACCAACGCCAAGATGAGCGAGCGCGCGCGCCCATGGCGCTCACTCCCTCGACGGGT	12109	
QY	977	TGTTGCGCTTCATCGCGCGCTTGGAGGAGCAGAAGGTGTGGACATCATCTGTCGCGGCC	1036	
Db	12108	TTCCCGAGGTTCATCGACCGGAACCGGGGCAACCGCGCGCTTACCGGAGCACCTCGGG	12049	
QY	1037	TGCCCAAGATPCTTGGCCACCGCCCAAGGTGCAGATCGGCATCTCTGGGTACCGGCAAGGCC	1096	
Db	12048	ACCTCCCGCGGTCTCTGTCGCGCGACCAAGACCGCCACGGCCCTCAACACCAACAGTACG	11989	
QY	1097	CCTACGAGAAGCTGTGTGAACGCCCATCGGCACCAAGTACAAGGGCGCGGCCAAGGCGGTGG	1156	

Db	11988	TTGATCGTGGAGATCAAGAGGCCACCAACCGGCATCCACCGGACCTCGTATGGAGGTCC	119929
Qy	1157	TCAAGTTCTCGGCGCCCTGGCGCACATGCTCACGGCCGGCGCGACTTTCATGCTGGTGC	1216
Db	11928	TGAAGGCCAAGGGGTGCACACCCGCGCTACTTCTCGCGGCTGCCACGAGCTGGAGC	11869
Qy	1217	CCTCGCGTTGAGCCCTGCGGCTGTATCCACTGCACGCCATGCACGTACGGTACCGTGC	1276
Db	11868	GGTACCGGGGAGCGACGACCGCCGCTGCCGACACACGAAAGCCCTCGCGCGCGGTGC	11809
Qy	1277	CCGTGGTAGCTCCACCGCGCGCTGGTGCACACGCTCAAGGAGGGCGGTACACGGCTTC	1336
Db	11808	TGTCCCTTCGGACCGGCACCGCATCGGGGACGACACATCCGCCGGTTCGCGACTGC	11749
Qy	1337	ACATGGGCGCCTGAACCCCGACAAGCTGGAGAGGCTGACGCGGACGCCCTGCGCCGCCA	1396
Db	11748	TCCGTCTCTGCGGACCCCGCGCGGAGTGCACCGCGGCCACCGGACACGCGCCCGC	11689
Qy	1397	CCGTGCGCGTCCCAACGAGGTGTTCGGGGCGCGCTATACCCCGAGATGGTGCCAACT	1456
Db	11688	CCCCGCTCGCGCCCC-----CAGACATCCACGCCCACTGTGACGCTCCCGA	11639
Qy	1457	GCATCAGCAGGACCTGTCTGTCTCAAGCCCGCCACAGAGTGGGAGGGCTGCTGGAGG	1516
Db	11638	TGACGCGCCCGCCCTTTCGGCACCGCCCGCGCGAAGCTGCGCGCACCCCGGAGCGC	11579
Qy	1517	AGTGTGTGTACGCAAGGGCGGTGGCCACCGCCAAAGAGGAGGAGATCAAGTGTGCCG	1576
Db	11578	ATCTGGGGCGGGTTCACGCCCTCGGCCACAGCCCTCGCCCGCGCGGCTGTCGCGCG	11519
Qy	1577	TTTCCGAGAGATCCCGGCGACTGCCCGCGGTGCTTACGGCCCCCAACACCTGAAGC	1636
Db	11518	CCGACGAGCCGGAACACGCGCGCCACCTCTCGCGGCTCGCGTTCGCGTACGGCAACA	11459
Qy	1637	CGGTGTCGCCTCCGTGGAGGGCAAGCGCGCCCGCGGCCACAGGTGGGACACACCGCC	1696
Db	11458	GGCCCTTCACCCCGCTGGAGAGGCGCGCACCTTGGCGTGCACCGGAGACGCTTCC	11399
Qy	1697	CCGCCATGGCGGTGGCGCGCACACCCCTCGGSCCCCTCGCCCGCGCGCCACCC	1756
Db	11398	GGCGCCTCTCTGCCCTTTTCGGGACGCTCCCGAGCTCCCGACCGCGGTTCAGACCGGCC	11339
Qy	1757	CCAAGGTGACCACTCAAGCCCGCCTGCGCGCACCGGCAAGCCCAAGACCGCTGGCC	1816
Db	11338	CCGCCGGGGTACTGGAAGAACACCTGTCTCCGCTCGAACACGCGGGGCTCTTCGACG	11279
Qy	1817	TCAAGTGGCGGTGAGGCCCTCCACCACTCGACCTCGGAGAACGGCGCTGCCCTCCACG	1876
Db	11278	CGCGCTCGCCAGGACCGCTCTTCCGCTACAGCGTGGCGCTTACCCGGCGCGGACCT	11219
Qy	1877	GCA 1879	
Db	11218	GCA 11216	

```

RESULT 15
US-09-861-289-3/c
; Sequence 3, Application US/09861289
; Patent No. US20020110897A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D. H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/861,289
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0

```


This Page Blank (uspto)

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1440	42.7	606	13	AA825476	Granule-bound star
2	1397.5	41.5	609	19	AAW56485	Oryza sativa starc
3	1390	41.2	527	21	AG044668	Arabidopsis thalia
4	1390	41.2	563	21	AAQ04667	Arabidopsis thalia
5	1390	41.2	610	21	AG046666	Arabidopsis thalia
6	1390	41.2	610	23	ABB91329	Herbicidially activ
7	1353.5	40.2	533	19	AAW56484	Zea mays waxy gene
8	1344.5	39.9	637	19	AAV16604	Protein encoded by
9	1331.5	39.5	502	13	AA825474	Central fragment f
10	1194	35.4	238	22	AA831175	A granule bound st

Claim 6; Page 28-33; 46pp; English.

A genomic library in *EMBL3* was prepared using leaves of the potato Bintje. The library was screened with cDNA clones for the 5' and 3' ends of the GSSS gene. A full-length clone of potato GSSS gene was identified (wx11) and isolated from the genomic library. The gene contained 12 introns. The amino acid sequence was deduced from it. Three fragments of the full-length sequence (5'-end, middle and 3'-end sequences) were characterised as suitable for use in novel antisense constructs to suppress amylose formation in potatoes. See also Q25400-3.

Db 545 KRAIKVVGTPAYEMVRNMCNODLSWKGPAKNWNL--LGLGVAGSAPGEGDEIAPLA 602
QY 519 KEIKVP 525
Db 603 KENVAAP 609

RESULT 3
AAG04668
ID AAG04668 standard; Protein; 527 AA.
XX
AC AAG04668;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 782.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 09-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135124.
PR 24-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139859.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144525.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 02-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.

PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 22-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.

```

PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 21-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match      41.2%; Score 1390; DB 21; Length 563;
Best Local Similarity 52.7%; Pred. No. 7.3e-101;
Matches 287; Conservative 72; Mismatches 146; Indels 40; Gaps 12;

QY 2 LDIVVAEVAEPWSTGGGLGVDYTGGLPIELVKRHRVMTIAPRQYADAWDTSVVVDI- 60
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
37 MSVIFGAEVGPWSTGGGLGVDYTGGLPPALAAARHRVMTICPRYDQYKDAWDTCCVVQIK 96
QY 61 MGEK---VYFHSIKGVURWIDHPFLAKVWGKTGSKLYGPRGADYLDNHKREALFC 117
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
97 VGDKEVNRFFHCYKRGVDRVFDHPIFLAKVVGKTGSKYIGPITGVNDYNDQLRFSLLC 156
QY 118 KAAIEAARVLPE-----GP-GECDVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA 169
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
157 QALAEAPQVNLNSSKYFSGPTGEDVVFVANDWHTALLPCYLKSMYQSRGVYNNAKVVEC 216
QY 170 IHNIAPQGRMEEAFKDTKLP---QAAFDKLAFSQGYAKVYTEATPMEDEKPLPGKYY 226
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 IHNIAYQGRFAFDYDLSLLNLPISFKSFD---FMDGYEK-----PVKG--- 256
QY 227 KINWLKGGIIAADKLVTVPNTATLADAGGVELDVIRAKGLEGVNGMDIEWNP 286
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
257 RKINWMAALEAHRLVLTSPYQAELISGVDGRGVELHLYRMTKTVSGIINGMDVQEWNP 316
QY 287 KTDKFLSAPYDQNSVYAGKAAKAEALQAEGLPVDPTAPLFAFTGLEQKGVDTIIAAL 346
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
317 STDKYIDIKYDITVTDAKPLIKEALQAAVGLPVDROPVPIGFIGRLEQKGSILVEAI 376
QY 347 PKLAPTKVOIALGTGKAAYEKLVAIGTKYKGRAGKVVVKSAPLAHMLTAGADFMVLP 406
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
377 SKPMGL-NVQMVLITGKKKMEAQILELEKFPKAGVAKFNVPLAHMITAGADFIIVP 435
QY 407 SRPEPGLIQLHAMHYGVTPVVASTGGLVTKGVTGFHMGALNP--DKLDEADADALA 464
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
436 SRPEPGLIQLHAMRYGVTPVIVASTGGLVTKGVTGFHMGALNP--DKLDEADADALA 495
QY 465 ATVRRASEVAGGRYEMPVANCIQSOLISWSPKQKWEGLLEEVYVYKGVVATAKKEIKV 524
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
496 KATRAVAVYGTSAQEMVKNQMDQFSNKKPARLWKKVLLSLNVA-GSEAGTEGEEL-A 553
QY 525 PVAEK 529
Db : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
554 PLAKE 558

RESULT 5
AAG04666
ID AAG04666 standard; Protein; 610 AA.
XX
AC AAG04666;
XX
DT 17-OCT-2000 (first entry)
XX

```

```

DE Arabidopsis thaliana protein fragment SEQ ID NO: 780.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.

```


Db	480	FEPCGLIQLOQMRYGTCACACASTGGLVDITIIIEGKTGFHMGRLSDVNCVVEPADVKKVATT	539
QY	467	VRRASEVAGRYPEMVANCISODLSWSKPAQKWEGLLEE--VYVGKGV-----ATAKK	519
Db	540	LQRAIKVVGTPAYEEMVRNCMIQDLSWKGPAKNWNLVLSLGVAGGEPGVEGEETAPLAK	599
QY	520	EEIKVP	525
Db	600	ENVAAP	605
RESULT 9			
ID	AAR25474	AAR25474 standard; Protein; 502 AA.	
XX	AC	AAR25474;	
XX	DT	15-JAN-1993 (first entry)	
XX	DE	Central fragment from potato GBSS.	
XX	KW	Granule-bound starch synthase; amylopectin; amylose production; inhibition.	
XX	OS	Solanum tuberosum.	
XX	PN	W09211376-A.	
XX	PD	09-JUL-1992.	
XX	PF	20-DEC-1991; 91WO-SE00892.	
XX	PR	21-DEC-1990; 90SE-0004096.	
XX	PA	(AMYL-) AMYLOGENE HB.	
XX	PI	Hofvander P, Persson PT, Tallberg A, Wikstrom O;	
XX	DR	WPI; 1992-250096/30.	
XX	DR	N-PSDB; AAQ26401.	
XX	PT	Modifying potatoes to form amylopectin starch - using an anti-sense construct to inhibit granule-bound starch synthase	
XX	PS	Claim 1; Page 21; 46pp; English.	
XX	CC	A genomic library in EMBL3 was prepared using leaves of the potato Bintje. The library was screened with cDNA clones for the 5' and 3' ends of the GBSS gene. A full-length clone of potato GBSS gene was identified (wx311). A BglII-SpeI fragment ("m") of the clone was found to contain the central region of the gene and was cloned in pUC13 to give pSm. Restriction of pSm with NsiI and HpaII gives fragment II which was cloned in pJRD184 to give pJRDmitt. Further restriction of pJRDmitt with HpaI-SstI gives a 2549bp fragment comprising exons and introns from the middle of the gene. The fragment can be used to make antisense constructs to suppress amylose formation in potatoes. See also Q26400-4.	
XX	SQ	Sequence	502 AA;
Query Match			
Best Local Similarity 39.5%; Score 1331.5; DB 13; Length 502;			
Matches 269; Conservative 55; Mismatches 125; Indels 35; Gaps 9;			
QY	2	LDIVMVAEYAPNSKGTGLDVTGGLEPIELVKGHRVMTIAPRYDQYADAWDSVVVDI-	60
Db	39	MNLIFVTEGVPWSKGTGLDVTGGLEPIELVKGHRVMTISPRDQKDAWDGTGVAEVK	98
QY	61	MG---EKVRYFHSIKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKRFAIFC	117
Db	99	VGDSIEIVRFHCYKRGVDRVFDHPFLEKMGKTSKLYGKAGLDYLDNLRFSILC	158
QY	118	KAATEAARVLFF-----GP-GEDCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLA	169

Db	159	QAALAPKVLNLSNSNYSGPYGEDVLFITANDWHTALIPCYLKSMYQSGIYLNKAVFC	218
QY	170	HNIAFOGRMWEAEFKDKLPQAFDKLAFSDGYAKVYTEATPMEDEKPPITGKTYKKI	229
Db	219	HNIAYQGRFSFSDPFLNLPDEFRCSPDFIDGY-----PVKG---RKI	259
QY	230	NWLKGIITAAADKLTVSPNYATEIADAAGGVLELDTVIRAKGIEGIVNGMDIEENPKTD	289
Db	260	NNMKAGILLESHRVTVSPYTAQELVSPVHKGYELDSVLKTKTCTGIVNGMDTQEWNPATD	319
QY	290	KFLSAPYD-QNSVYAGKAAKALQALGLPVDPTAPLFAFTIGRLEEQGVDIILAAALPK	348
Db	320	KYTDVKYDITQVMDAKPLLEKALQAVGLPVDKWKIPLIGFICRLEEQGSDILVAIIHK	379
QY	349	ILATPKVQIAILGTGKAAYEKLNVNAITGTYKGRAGVVKFSAPLAHMLTAGADFMVPSR	408
Db	380	FIGL-DVQIVVLGTGCKEFEQIEQLEVLVPHKAGVAKFNVPLAHMITAGADFMVPSR	438
QY	409	FEPCGLIQLOHAMHYGVVAVSTGGLYVDIVKGVTFGHMGALNP--DKLDEADADAAT	466
Db	439	FEPCGLIQLOHAMRYGTVPICASTGGLVDIVKGVTFGHMGAFNVECDVVDPAVLKIVT	498
QY	467	VRRA	470
Db	499	VARA	502
RESULT 10			
ID	AAB31175	AAB31175 standard; Protein; 238 AA.	
XX	AC	AAB31175;	
XX	DT	02-APR-2001 (first entry)	
XX	DE	A granule bound starch synthetase II (GBSSII).	
XX	KW	Granule bound starch synthetase II; GBSSII; starch grain;	
XX	KW	adenosine diphosphate glucose-alpha1,4-glucan alpha4-glucosyltransferase; starch synthetase.	
XX	OS	Chlamydomonas reinhardtii.	
XX	PN	FR2793806-AL.	
XX	PD	24-NOV-2000.	
XX	PF	21-MAY-1999; 99FR-0006494.	
XX	PR	21-MAY-1999; 99FR-0006494.	
XX	PA	(CNRS) CNRS CENT NAT RECH SCI.	
XX	PI	Dhulst C, Ball S;	
XX	DR	WPI; 2001-052291/07.	
XX	DR	N-PSDB; AAC86955.	
XX	PT	New recombinant nucleic acid encoding fusion of starch synthase and second component, useful in pharmaceutical and food compositions, is targeted to starch granules -	
XX	PS	Claim 9; Fig 1; 52pp; French.	
XX	CC	The present sequence represents a granule bound starch synthetase II (GBSSII). The specification describes a recombinant nucleic acid, comprising a polynucleotide encoding an adenosine diphosphate glucose-alpha1,4-glucan alpha4-glucosyltransferase of starch synthetase, placed upstream of a sequence that encodes a polypeptide of interest. The adenosine diphosphate glucose-alpha1,4-glucan alpha4-glucosyltransferase protein can migrate to sites of biosynthesis of starch grains in plant cells, becoming associated	

CC with these grains. The recombinant nucleic acid sequence is used to
 CC target polypeptides of interest to starch grains.
 XX

SQ Sequence 238 AA;

Query Match 35.4%; Score 1194; DB 22; Length 238;
 Best Local Similarity 99.2%; Pred. No. 5.9e-86;
 Matches 234; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 416 QIHAMHYGVTPVASTGGLVDVTKGVTGFHMGALNPKDLDEADADALAATVRRASEVEFA 475
 DB :::
 3 RVHAMHYGVTPVASTGGLVDVTKGVTGFHMGALNPKDLDEADADALAATVRRASEVEFA 62
 QY 476 GGRYPFEMVANCISQDLSSKPAQKWEGLLEEVYKGGVATAKKEIKVPVAEKIPGDLP 535
 DB :::
 63 GGRYPFEMVANCISQDLSSKPAQKWEGLLEEVYKGGVATAKKEIKVPVAEKIPGDLP 122
 QY 536 AVSYAPNTLKPVSASVEGNGAAAPKVGTTAPAMGAWRATTPSGPSPAAATPKVTYKPAL 595
 DB :::
 123 AVSYAPNTLKPVSASVEGNGAAAPKVGTTAPAMGAWRATTPSGPSPAAATPKVTYKPAL 182
 QY 596 PATAKPKTAGIKLAGEASTTSTSENGAASNGNGASASKTSAAKPLVSAATRKA 651
 DB :::
 183 PATAKPKTAGIKLAGEASTTSTSENGAASNGNGASASKTSAAKPLVSAATRKA 238

RESULT 11

AAB49307
 ID AAB49307 standard; Protein; 534 AA.

XX AC AAB49307;

XX DT 01-MAR-2001 (first entry)

XX DE Wheat starch synthase GRSS protein.

XX KW Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
 XX food product; adhesive.

XX OS Triticum aestivum.

XX PN WO200066745-A1.

XX PD 09-NOV-2000.

XX PF 28-APR-2000; 2000WO-AU00385.

XX PR 29-APR-1999; 99AU-0000052.

XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX PA (GOOD-) GOODMAN FIELDER LTD.

XX PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX PI Morell M, Li Z, Rahman S, Appels R;

XX DR WPI; 2000-647602/62.

XX PT Nucleic acid molecules encoding wheat starch synthase (WST)-I and
 XX WST-II, useful in modifying plant starch content and/or composition -

XX PS Example 15; Fig 9; 21lpp; English.

XX The present invention relates to novel protein and coding sequences from
 CC wheat. The proteins are wheat starch synthases, designated SSII and
 CC SSIII. These can be used in the modification of plant starch content or
 CC composition, and to screen plants to identify mutations which affect
 CC starch content and composition. The starch can then be used in food
 CC products, such as flour, and in films, coatings, adhesives, building
 CC materials and packaging materials.

XX SQ Sequence 534 AA;

Query Match 26.8%; Score 904; DB 21; Length 534;

Best Local Similarity 32.5%; Pred. No. 1.4e-62;
 Matches 213; Conservative 48; Mismatches 103; Indels 292; Gaps 9;

QY 7 VAAEVAPWSKTGGLGDTGTLPIELVKRGHVRMTIAPRDOYADADNTSVVDIMGEKVR 66
 DB :::
 2 VQAEAPWSKTGGLGDLGLGPPMAAANGHRVMTISPRYDQYKADWDT----- 49
 QY 67 YFHSIKKGVRHVMIDHPWFLAKWGTGSKLYGPRSGADYLDNHHKFAFLFCKAAIBAAVR 126
 DB :::
 50 -----LEKVRGKTEKIKYGPDACTYEDNQRFSLCQAALFVPRI 90
 QY 127 L-----PF----- 129
 DB :::
 91 LNLNPNPYFCIHNIISYQGRFSFDDPAQLNLPDRFKSSFDFIDGYDKPVEGRKISVVSEI 150
 QY 130 -----GP-GEDCVFVANDHWSALVPVLLKDEYQPK 158
 DB :::
 151 KVVDKYRVRYPHCYKRGVDRVFDHPGSPGYGEDVFCVNDWHTGLLACYLKSNYQSN 210
 QY 159 GQFTKAKSVLAHNIAPQGRMWEAPKDTKLPAAPDKLAFSDGYAKVYVTEATPMEDEK 218
 DB :::
 211 GIYRAAKVA----- 219
 QY 219 PPLTKYTKYKINWLKGGIITADKLVTSYNYATEIAADAAGVGLDVIIRAKGIEGIVNG 278
 DB :::
 220 -----NWMKAGILQADKVLTVSPYAFELISGEARGCELDNIMRLTGITTVNG 268
 QY 279 MDIEEWNPKTKPLSAPYDONSAYAKAAK----- 309
 DB :::
 269 MDVSEWDPKTKPLAVNYDITTALEKGLNKLKALEKALNKLKEEDVQIVLGTGKKKPE 328
 QY 310 -----EALQAEELGVPDTPAPLFAFIFGRLEEOKGVDTILA 344
 DB :::
 329 RLLKSTIEKFPKSVRAVVRFNAPLAEALQAEVGLPVDKRVPLVAFIFGRLEEOKGVDTILA 388
 QY 345 ALPKILATPKVOIAILGTGKAAAYEKLNVNAIGTKYKRAKGVVYKFSAPLAHMLTAGADFML 404
 DB :::
 389 SIPEI-----HOMMAGADVLA 404
 QY 405 VPSREFPCGLIOLHAMHYGVTPVAVASTGGLVDVTKGVTGFHMGALNPD--KLDADADA 462
 DB :::
 405 VTSREFPCGLIOLQGMRYGTPCACASTGGLVDVTKGVTGFHMGALNPDVNVVEPADVKK 464
 QY 463 LAAIVRRASEVFPAGGRYPE-----MVANCISQDLSSKPAQKWEGLLEEV 507
 DB :::
 465 VVTILKRAVKVVGTPAYHEAPLAMEVNAAPMYKNCMIQDLSSKPAKKNWEDVLEL 520

RESULT 12

ABB92160

ID ABB92160 standard; Protein; 792 AA.

XX AC ABB92160;

XX DT 31-MAY-2002 (first entry)

XX DE Herbicidally active polypeptide SEQ ID NO 1371.

XX KW Herbicidal; plant; agriculture; herbicide.

XX OS Arabidopsis thaliana.

XX PN WO200210210-A2.

XX PD 07-FEB-2002.

XX PF 28-AUG-2001; 2001WO-EP09892.

XX PR 28-AUG-2001; 2001WO-EP09892.

XX PA (FARB) BAYER AG.

XX PI Tietjen K, Weidner M;

Db 420 DKCLPHYSVDDL-SGKAKCKALQELGLPVREDVPLIGFICRLDYQKGLIDLIKMAIPE 478
 QY 349 ILATPKVQIAILGTGKAAEKLNAIGTKYKRAKGVKFSAPLAHMLTAGADFMVPSR 408
 Db 479 LM-REDVQVFMGLSGDPIFEGWNRSTESSYKDKFRGWGFSVPVSHRITAGCDILLMP 537
 QY 409 FPCGLIQLHAMHYGVPVASTGGGLVDTVK-----EGVTGFHMGALNPDKLDEAD 459
 Db 538 FPCGLNQLYAMQYGVVPHVHGGLGURDTVETNPFCAKGEETGWAFSPLTVDKMLWAL 597
 QY 460 ADALATVRRASEVFAGGRYPENVANCISQDLSWSKPAQKWEGILLE 505
 Db 598 RTAM-STEREHKSWSG-----LMKRGMTKDHWDHAAEQYEQIFE 637

RESULT 14

AAW38218
 ID AAW38218 standard; Protein; 649 AA.

XX
 AC AAW38218;

XX
 DT 22-MAY-1998 (first entry)

XX
 DE Maize starch synthase type I.

XX
 KW Maize; starch synthase type I; starch.

XX
 OS Zea mays.

XX
 PN DE19619918-Al.

XX
 PD 20-NOV-1997.

XX
 PF 17-MAY-1996; 96DE-1019918.

XX
 PR 17-MAY-1996; 96DE-1019918.

XX
 PA (PLAN-) PLANTTEC BIOECONOLOGIE GMBH.

XX
 PI Froberg C, Kossmann J;

XX
 WPI; 1998-000821/01.

DR N-PSDB; AAT95785.

XX
 PT DNA encoding maize starch synthase type I protein - for producing

PT transgenic plants

XX
 PS Claim 1; Pages 16-20; 23pp; German.

XX The present sequence is maize starch synthase type I, useful
 CC in the production of starch. Starch can be used in various
 CC conventional starch applications, e.g. starch hydrolyzate products,
 CC foods, papermaking, adhesives, textiles, building materials, soil
 CC stabilisation, agrochemicals, pharmaceuticals, cosmetics, coal
 CC briquettes, ore and coal slurries, foundry casting, rubber, leather
 CC and synthetic polymers. The enzyme produces a starch stated to have
 CC different physicochemical properties, especially viscosity and
 CC gelling properties, from wild type starch.

XX
 SQ Sequence 649 AA;

Query Match

Best Local Similarity 26.2%; Score 882.5; DB 19; Length 649;

Matches 203; Conservative 95; Mismatches 174; Indels 57; Gaps 15;

QY 3 DIVMVAAEYAPWSKGGGLDVTGGLPIELVKRGHVRMTIAPRY-----DQYADAWDISV 56

Db 142 NIVFTGASPYAKSGGLDVGCSLPVALAARGHVRVMVMPRLNGTSDKNYANAFYTEK 201

QY 57 VVDIM---GE-KVRYFHSIKKGVHRWIDHPWFLAKVWGKSGKLYGPRSGADYLDNHR 112

Db 202 HIRIPCFGGEHVTFFHEYRSDVDMVFVDHPFSY-----HRPGNLYGDKFGA-FGDNOFR 254

QY 113 FALFCKAAIEAARVLPFGP---GEDCVFVANDHSAIVPVLKDEYQPKGFTKAKSVLA 169
 Db 255 YTLCCYAAACEAPLVLEGGYIYGNCFVNDHSAIVPVLKAAKYRYPGYKDRSILV 314
 QY 170 IHNIAQGRWEAEAFDKLPQAAFDKLAISDGYAKYVYVTEATPMEDEKPLTGKTYKKI 229
 Db 315 IHNLAHGGVBPASTYDGLGPPPEWYGALEW-----VFPEWARRHALDKG-----EAV 361
 QY 230 NMLKGGIITADKLVTVSPNYATEIADAAGSVELDTVI--RANGIEGIVNGMDIEENPK 287
 Db 362 NFLKGAIVADRIYTVSKSGSWETT-AEGQGLNELLSRKSXVNLVINGIINDWNPA 420
 QY 288 TDKELSAFYDQNSVYAKAAKALQAEGLPVDPTAPLFAFICRLEEQKGVDTILAAALP 347
 Db 421 TDKCIPCHYSVDDL-SGKAKCKGALQKELGPIRPDVPVLIGFICRLDYQKGLIDLIIP 479
 QY 348 KILATPKVQIAILGTGKAAEKLNAIGTKYKRAKGVKFSAPLAHMLTAGADFMVPS 407
 Db 480 DLM-REDVQVFMGLSGDPELEDWNRSTESIFKDKFRGWGFSVPVSHRITAGCDILLMP 538
 QY 408 REPCGLIQLHAMHYGVPVASTGGGLVDTVK-----EGVTGFHMGALNPDKLDEA 458
 Db 539 REPCGLNQLYAMQYGVVPHVHGGLGURDTVETNPFCAKGEETGWAFSPLTV 594
 QY 459 DADALATVRRASEVFAGGR--YPMVANCISQDLSWSKPAQKWEGILLE 505
 Db 595 ---MLWTLTKTAISTYREHKSSWEGMLKRCMSKDFTDHAAEQYEQIFQ 639

RESULT 15

AAW23937
 ID AAW23937 standard; Protein; 671 AA.

XX
 AC AAW23937;

XX
 DT 21-MAY-1998 (first entry)

XX
 DE Wheat soluble starch synthase partial sequence.

XX
 KW Starch synthase; wheat; transgenic plant.

XX
 OS Triticum aestivum L. cv. Florida.

XX
 PN W09745545-Al.

XX
 PD 04-DEC-1997.

XX
 PF 28-MAY-1997; 97WO-EP02793.

XX
 PR 11-SEP-1996; 96DE-1036917.

XX
 PR 29-MAY-1996; 96DE-1021588.

XX
 PA (AGRE) HOECHST-SCHERING AGREVO GMBH.

XX
 PI Block M, Loerz H, Luetticke S, Froberg C, Kossmann J;

XX
 PI Walter L;

XX
 DR WPI; 1998-032652/03.

XX
 DR N-PSDB; AAV01527.

XX
 PT Nucleic acid encoding starch synthase enzymes from wheat - for

PT transgenic plants that produce modified forms of starch, useful e.g.

PT in foods, or for production of packaging materials and disposable

XX
 goods

XX
 PS Claim 1; Page 47-50; 71pp; English.

XX This amino acid sequence comprises a near full-length sequence for
 CC a soluble starch synthase of summer wheat (cv. Florida). It was
 CC deduced from a cDNA clone (AAV01527) isolated from a 21-day caryopsis
 CC cDNA library. A granule-bound starch synthase (see AAW23938) has
 CC also been identified. Isolated nucleic acids encoding these
 CC enzymes can be inserted into vectors for production of transgenic

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: June 4, 2003, 14:47:01 ; Search time 16.8268 Seconds
(without alignments)
3719.278 Million cell updates/sec

Title: US-09-980-771a-5
Perfect score: 3370
Sequence: 1 ALDIVVAAEVAWPSKTTGGL.....SASKTSAKPLVSAATRKA 651

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PTR_73:*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1481.5	44.0	608	2	S43341	starch synthase (E
2	1457.5	43.2	607	1	TOPOX	starch synthase (E
3	1415.5	42.0	603	2	S61504	glycogen(starch) s
4	1412.5	41.9	608	2	T10906	starch synthase (E
5	1398.5	41.5	609	2	J00703	glycogen(starch) s
6	1397.5	41.5	609	2	S11481	glycogen(starch) s
7	1395.5	41.4	603	1	Y0BHY	glycogen(starch) s
8	1390	41.2	610	2	F86453	granule-bound star
9	1362	40.4	615	1	Y0WYX	glycogen(starch) s
10	1355.5	40.2	608	2	T14731	glycogen(starch) s
11	1353.5	40.2	605	1	S07314	glycogen(starch) s
12	1194	35.4	238	2	T07921	probable starch sy
13	902.5	26.8	641	2	T07668	starch synthase (E
14	873.5	25.9	626	2	T02322	starch synthase (E
15	872	25.9	732	2	T01208	starch synthase (E
16	871	25.8	752	2	S61505	probable starch sy
17	869	25.8	610	2	T06280	probable starch sy
18	861.5	25.6	622	2	T01414	starch synthase (E
19	847.5	25.1	788	2	T07667	glycogen(starch) s
20	839	24.9	491	2	T06798	probable starch sy
21	837	24.8	698	2	T01209	starch synthase (E
22	684.5	20.3	477	2	B95130	glycogen synthase
23	683.5	20.3	477	2	H98000	starch synthase (E
24	677.5	20.1	484	2	S40051	starch synthase (E
25	669	19.9	483	2	C86712	starch synthase (E
26	652	19.3	480	2	H98228	glycogen synthase
27	651	19.3	480	2	AF3057	glycogen synthase
28	651	19.3	486	2	H72321	glycogen synthase
29	637	18.9	477	2	A97176	glycogen synthase,

30 622 18.5 484 2 F82165 glycogen synthase
31 614.5 18.2 476 2 E83785 starch (bacterial
32 604.5 17.9 486 2 C96018 probable starch sy
33 604 17.9 476 2 AE0479 starch synthase (E
34 590.5 17.5 530 2 AH3194 glycogen synthase
35 587 17.4 477 1 SYECGL starch synthase (E
36 587 17.4 477 2 B98163 glycogen synthase
37 587 17.4 477 2 C86009 glycogen synthase
38 587 17.4 477 2 AI0995 starch synthase (E
39 569 16.9 476 2 C64119 starch synthase (E
40 568.5 16.9 1230 2 T07663 soluble starch syn
41 561.5 16.7 1025 2 H86250 hypothetical prote
42 560.5 16.6 472 2 AI2040 glycogen synthase
43 552.5 16.4 463 2 C70363 glycogen synthase
44 536 15.9 492 2 AG1810 glycogen (starch)
45 535 15.9 477 2 S76496 hypothetical prote

ALIGNMENTS

RESULT 1

S43341

starch synthase (EC 2.4.1.21) precursor - cassava

N:Alternate names: bacterial-glycogen synthase; glycogen synthase; starch synthase
C:Species: Manihot esculenta (cassava)

C>Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2002

C:Accession: S43341

R:Salehuzzaman, S.N.I.M.; Jacobsen, E.; Visser, R.G.F.

Plant Mol. Biol. 23, 947-962, 1993

A:Title: Isolation and characterization of a cDNA encoding granule-bound starch synth

A:Reference number: S43341; MUID:94083565; PMID:8260633

A:Accession: S43341

A:Molecule type: mRNA

A:Residues: 1-608 <SAL>

A:Cross-references: EMBL:X74160; NID:g437041; PIDN:CAA52273.1; PID:g437042

C:Genetics:

A:Gene: GBSS; waxy

A:Genome: nuclear

C:Function:

A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producin

C:Superfamily: starch synthase

C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltra

F:1-78/Domain: transit peptide (amyloplast) #status predicted <TNP>

F:79-608/Product: ADPglucose-starch glucosyltransferase #status predicted <MAT>

Query Match

Best Local Similarity 44.0%; Score 1481.5; DB 2; Length 608;

Matches 299; Conservative 64; Mismatches 148; Indels 33; Gaps 9;

QY 2 LDIYVAAEVAWPSKTTGGLDVTGGLPIELVKRHRVMTIAPRYDOYADADMTSVVVDI- 60
Db 82 MNLIFVCAEVPWSKTTGGLDVTGGLPIELVKRHRVMTIAPRYDOYADADMTSVVVDI- 141
QY 61 MG---EKVYRPHSTKKGVRHVRWIDHPWFLAKWVGKTGSKLYGPRSGADYLDNHRKFALEFC 117
Db 142 IGDRIETVRFPHSKRGVDRVDFVDPMPLEKVGWGTGSKLYGPRAGLDYQDNQLRSLC 201
QY 118 KAAEAAARVLFP-----GP-GEDCVVANDWHSALVPVLLKDEYQPKGFTKAKSVLA 169
Db 202 LAALAEPRVNLNSKNFSGPYGEVAFIANDWHTALIPCYLKAIYQPMGIYKHAFAVC 261
QY 170 IHNIAFGRWEEAFKDTKLPQAAFDKLAFSKGAKYVTEATPMEDEKPLTKTKYKKI 229
Db 262 IHNIAFGRAFSDFPRLNLPDKFSFDFIDGYE-----PVKG---RKI 304
QY 230 NNLKGGIADKNTVSPNTATETADAAGGVELDTVIRAKGIEGVNGMDIEENPKTD 289
Db 305 NWMKAGILESRLVTSPPYTAQAEIVSGVERGVLDNERTKGTGIAIINGMDVQENPVD 364
QY 290 KFLSAPYDQNSVYAGKAAKAEALQAEGLPVDPTAPFATIGRLEEGKGVDDIILALPKI 349
Db 365 KYIDHYDATTVMDDAKPFLKAEALQAEGLPVDNRVPLTIGFIRLEEGKGSDFVAAISQ- 423

Db 197 QAALAPRVNLNNSKYSFGPYGEDIYFVANDHWSALIPCYLKSWMYKSRGLYKNAKVAFC 256
 QY 170 IHNIAFOGRMWEBAFKD---TKLPQAAFDKLAESDGYAKVYVTEATPMEDEKPLTGTCTY 226
 Db 257 IHNIAOGR---NAFSDFLNLPDEPRSSDFIDGYNK-----PCEG--- 296
 QY 227 KKNLWKGGLIADKLVTSFVSPNATEIAAAGGVELDTVIRAKGIEGIVNGMDIEWNP 286
 Db 297 KKNLWKGGLIADKLVTSFVSPNATEIAAAGGVELDTVIRAKGIEGIVNGMDIEWNP 356
 QY 287 KTKFSLAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFGRLEEGKGVDIILAAAL 346
 Db 357 QTDRIYDHYNEITYEAKPLKGLTQAEGLPVDSSIPILGFGIRLEEGKGVDIILVFAI 416
 QY 347 PKILATPKVOIALIGTGAAYEKLIVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVLP 406
 Db 417 AK-FADENVOIVLGTGKTKMEQKIELEEKYKGAIGTKFNSPLAHKIAGADFVIP 475
 QY 407 SRPEPCGLIOLHAMHYGTVPVASTGGLVDTVKEGVTGFHMGALNP--DKLDEADADALA 464
 Db 476 SRPEPCGLIOLHAMHYGTVPVASTGGLVDTVKEGVTGFHMGALNP--DKLDEADADALA 535
 QY 465 ATVRRASEVFAGGRYPENVANCISQDLSWSKPAOKWEGLLFV-----VYKGG--VATA 517
 Db 536 ATKRALKTYGTQAMKQIILNCMAQNFSSWKKPAKLWEKALLNLEVTGNVAGIDGDEIAPL 595
 QY 518 KKEIKVP 525
 Db 596 AKENVATP 603

RESULT 4

Tl0906
 starch synthase (EC 2.4.1.21) - sweet potato
 N:Alternate names: starch synthase
 C:Species: Ipomoea batatas (sweet potato)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002
 C:Accession: Tl0906
 R:Wang, S.J.; Yeh, K.W.; Tsai, C.Y.
 Submitted to the EMBL Data Library, December 1995
 A:Reference number: Z17212
 A:Accession: Tl0906
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-608 <WAN>
 A:Cross-references: EMBL:U44126; NID:g1172158; PID:g1172159
 A:Experimental source: cv. Tainong; tuberous root
 C:Genetics:
 A:Gene: SS67
 C:Function:
 A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing a
 A:Pathway: starch biosynthesis
 C:Superfamily: starch synthase
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 41.98; Score 1412.5; DB 2; Length 608;
 Best Local Similarity 53.58; Pred. No. 6e-77;
 Matches 292; Conservative 61; Mismatches 152; Indels 41; Gaps 10;
 QY 2 LDIWVAAEAVAPWSKTTGGLGVTGGLPIELVKRGHVRWMTIAPRYDQYADAWDTSVVD-I 60
 Db 82 MNLVFCGCEGCPWCKTGGGLGVLGGLPALAARHVRWTCPRDQYADAWDTSVVD-I 141
 QY 61 MG---EKVRVPHSKGVRHWIDHPWFLAKVWCKTSGKLYGPRSGADYLDNHRKRALFC 117
 Db 142 VGDRIEYRFRPHSKGVRHWIDHPWFLAKVWCKTSGKLYGPRSGADYLDNHRKRALFC 201
 QY 118 KAALAEARVLPF-----GP-GEDCVFVANDHWSALVPLVKDEYQPKGFTTAKSVLA 169
 Db 202 QAALAEARVNLNNSKYSFGPYGEDIYFVANDHWSALVPLVKDEYQPKGFTTAKSVLA 261
 QY 170 IHNIAFOGRMWEBAFKDITKLPQAAFDKLAESDGYAKVYVTEATPMEDEKPLTGTCTY 229

Db 262 IHNIAOGRPAFSDPSLLNLPDEYKGSFDFIDGTDK-----PVKG---RKI 304
 QY 230 NNLKGGIIAADKLVTSFVSPNATEIAAAGGVELDTVIRAKGIEGIVNGMDIEWNP 289
 Db 305 NNMKAGIREADRVFTSPNYAKELVSCVSKGVDELNDHIDCGITGICNGMDTQWNPATD 364
 QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFGRLEEGKGVDIILAAALPKI 349
 Db 365 KYLAVKDYDITVMQAKPLLEALQAAVGLPVDRIPLTIGFGRLEEGKGVDIILAAALSKF 424
 QY 350 LATPKVOIALIGTGAAYEKLIVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVLP 409
 Db 425 ISM-DVQILLIGTGGKFFEQIEQLEVMYPDKRGVAKFNPLAHMITAGADFMVLP 483
 QY 410 EPCGLIOLHAMHYGTVPVASTGGLVDTVKEGVTGFHMGALNP--DKLDEADADALA 467
 Db 484 EPCGLIOLHAMHYGTVPVASTGGLVDTVKEGVTGFHMGALNP--DKLDEADADALA 543
 QY 468 RASEVFAGGRYPENVANCISQDLSWSKPAOKWEGLLFV-----EYVYKGGVATAKK 519
 Db 544 GRALATYGTGTAFTTEMKNCMSQELSWKGPKNWETVLISLGVAGSEPGVEGE-ETAPLAK 602
 QY 520 BEIKVP 525
 Db 603 ENVATP 608

RESULT 5
 JQ0703
 glycogen(starch) synthase (EC 2.4.1.11) - rice
 N:Alternate names: granule-bound starch synthase
 C:Species: Oryza sativa (rice)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-2002
 C:Accession: JQ0703
 R:Wang, Z.Y.; Wu, Z.L.; Xing, Y.Y.; Zheng, F.G.; Guo, X.L.; Zhang, W.G.; Hong, M.M.
 Nucleic Acids Res. 18, 5898, 1990
 A:Title: Nucleotide sequence of rice waxy gene.
 A:Reference number: JQ0703; MUID:91016948; PMID:2216792
 A:Accession: JQ0703
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-609 <WAN>
 A:Cross-references: EMBL:X53694
 A:Experimental source: strain subsp. japonica Hengfeng
 C:Genetics:
 A:Gene: waxy
 A:Introns: 114/1; 141/1; 174/1; 204/1; 225/2; 259/1; 295/3; 377/1; 436/1; 500/1; 529/1
 C:Function:
 A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose producing a
 C:Superfamily: starch synthase
 C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 41.58; Score 1398.5; DB 2; Length 609;
 Best Local Similarity 51.28; Pred. No. 4.1e-76;
 Matches 280; Conservative 77; Mismatches 147; Indels 43; Gaps 9;
 QY 2 LDIWVAAEAVAPWSKTTGGLGVTGGLPIELVKRGHVRWMTIAPRYDQYADAWDTSVVD-I 60
 Db 83 MNLVFCGCEGCPWCKTGGGLGVLGGLPALAARHVRWTCPRDQYADAWDTSVVD-I 142
 QY 61 ---MGEKVRVPHSKGVRHWIDHPWFLAKVWCKTSGKLYGPRSGADYLDNHRKRALFC 117
 Db 143 VADRIEYRFRPHSKGVRHWIDHPWFLAKVWCKTSGKLYGPRSGADYLDNHRKRALFC 202
 QY 118 KAALAEARVLPF-----PFGP---GEDCVFVANDHWSALVPLVKDEYQPKGFTTAKSVLA 169
 Db 203 QAALAEARVNLNNSKYSFGPYGEDIYFVANDHWSALVPLVKDEYQPKGFTTAKSVLA 262
 QY 170 IHNIAFOGRMWEBAFKDITKLPQAAFDKLAESDGYAKVYVTEATPMEDEKPLTGTCTY 229
 Db 263 IHNIAOGRPAFSDPSLLNLPDEYKGSFDFIDGTDK-----DTPVEG-----RKI 305
 QY 230 NNLKGGIIAADKLVTSFVSPNATEIAAAGGVELDTVIRAKGIEGIVNGMDIEWNP 289

```

Db 306 NMWAGILADRVLTSPYAAELISGARGCELDNIMRLTGTIGVNGMDVSEWPSKD 365
QY 290 KFLSAPYDQNSVYAGAAKAEALQAEGLPVDPTAPLFAFGLRLEQKGVDDIILALPKI 349
Db 366 KYITAKYDATTAEAKALKEALQAEAGLPVDRKIPLIAPFGLRLEQKGVDDIILALPKI 425
QY 350 LATPKVQJAILLGTGKAAEYKLVNAIGTKYKGRAGKGVVVFSAPLAHMLTAGADPMLVPSRF 409
Db 426 M-QEDVQIVLLGTGKKFELKLSMEEKYPGKVRVAVVKNAPLAHLIMAGADVLPVPSRF 484
QY 410 EPGGLIQLHAMHYGTVPVVAAGTGLVDTVKEGVTGFHMGALNPD--KLEADADALAATV 467
Db 485 EPGGLIQLQCMRYGTACACASTGGLVDTVIEGKTGFHMGRLSDGVKVPVSDVKKVAATL 544
QY 468 RASEVFAGGRYPPEMVAANCISODLSWSKPAQKWEGLLEEVYVYKGG-----VATAK 518
Db 545 KRAIKVVGTPAYEEMVRNQNQLSWKGFKNWENVL--LGLGVAGSAPGIEGDEIAPLA 602
QY 519 KEIKVP 525
Db 603 KENVAAP 609

```

RESULT 6

```

S11481
glycogen(starch) synthase (EC 2.4.1.11) precursor - rice
N;Alternate names: starch synthase; waxy protein
C;Species: Oryza sativa (rice)
C;Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2002
C;Accession: S11481; S22519; S30485; PC2190; JQ2224
R;Wang, Z.Y.; Wu, Z.L.; Xing, Y.X.; Zheng, F.G.; Guo, X.L.; Zhang, W.G.; Hong, M.M.
Nucleic Acids Res. 18, 5898, 1990
A;Title: Nucleotide sequence of rice waxy gene.
A;Reference number: JQ0703; MUID:91016948; PMID:2216792
A;Accession: S11481
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-609 <WAX>
A;Cross-references: EMBL:X53694; NID:g577598; PIDN:CAA37732.1; PID:g577599
R;Okagaki, R.J.
Plant Mol. Biol. 19, 513-516, 1992
A;Title: Nucleotide sequence of a long cDNA from the rice waxy gene.
A;Reference number: S22519; MUID:92322986; PMID:1377969
A;Accession: S22519
A;Molecule type: mRNA
A;Residues: 1-609 <OKA>
A;Cross-references: EMBL:X62134; NID:g20402; PIDN:CAA44065.1; PID:g20403
R;Hirano, H.Y.; Sano, Y.
Plant Cell Physiol. 32, 989-997, 1991
A;Title: Molecular characterization of the waxy locus of rice (Oryza sativa).
A;Reference number: S30485
A;Accession: S30485
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-609 <HR>
A;Cross-references: EMBL:X58228; NID:g20400; PIDN:CAA41186.1; PID:g20401
A;Accession: PC2190
A;Molecule type: protein
A;Residues: 78-113 <HI2>
A;Experimental source: leaf, cDNA pOSLHC2120
C;Comment: This protein is involved in amylose synthesis in the rice endosperm.
C;Genetics:
A;Gene: waxy
A;Introns: 113/3; 140/3; 173/3; 203/3; 225/1; 258/3; 295/2; 376/3; 435/3; 499/3; 528/3;
C;Function:
A;Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose producing
A;Pathway: starch biosynthesis
A;Superfamily: starch synthase
C;Keywords: amyloplast; chloroplast; glycogen/starch biosynthesis; glycosyltransferase;
F;1-77/Domain: transit peptide (amyloplast) #status predicted <TNP>
F;78-609/Product: glycogen (starch) synthase #status experimental <MAN>

```

```

Query Match 41.5%; Score 1397.5; DB 2; Length 609;
Best Local Similarity 51.4%; Pred. No. 4.7e-76;
Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;

QY 2 LDIVMVAEAVAPWSKTGGLGVGTGGLPIELVKGRHVRMTIAPRYDQYADAWDTSVVVDI- 60
Db 83 MNVVFVGAENAPWSKTGGLGVGLPPAMAANGHRVWVSPRYDQYKDAWDTSVVAEIK 142
QY 61 ---MGEKVRVFEHSTIKGVHVRVLDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
Db 143 VADRYEKRVFEHFKYKRGVDRVFIDHPSELEKVGWKTGKIYGPDTGVYDKDNQMRFLLC 202
QY 118 KAAEAAARVL-----PEGP---GEDCVFVANDHESALVPVLLKDEYOPKGFQAKASVLA 169
Db 203 QAALEAPRIILNNPNPYKGTGYEDVVVCNDHWTGTPLASLYKNNYQNGIYRNKAVAF 262
QY 170 IHNIAFOGRWWEAFKDTKLPOAFAFDKLAISDGYAKVYTEATPMEEDEKPLGKTYKKI 229
Db 263 IHNISYOGRAFEDYPELNLSERFSRSDFDIGY-----DTPVEG-----RKI 305
QY 230 NNLKGGIIAADKLVTSPNYATEIAADAAGGVVELDTVIRAKGTGIVNGMDIERNPKTD 289
Db 306 NMWAGILADRVLTSPYAAELISGARGCELDNIMRLTGTIGVNGMDVSEWPSKD 365
QY 290 KFLSAPYDQNSVYAGAAKAEALQAEGLPVDPTAPLFAFGLRLEQKGVDDIILALPKI 349
Db 366 KYITAKYDATTAEAKALKEALQAEAGLPVDRKIPLIAPFGLRLEQKGVDDIILALPKI 425
QY 350 LATPKVQJAILLGTGKAAEYKLVNAIGTKYKGRAGKGVVVFSAPLAHMLTAGADPMLVPSRF 409
Db 426 M-QEDVQIVLLGTGKKFELKLSMEEKYPGKVRVAVVKNAPLAHLIMAGADVLPVPSRF 484
QY 410 EPGGLIQLHAMHYGTVPVVAAGTGLVDTVKEGVTGFHMGALNPD--KLEADADALAATV 467
Db 485 EPGGLIQLQCMRYGTACACASTGGLVDTVIEGKTGFHMGRLSDGVKVPVSDVKKVAATL 544
QY 468 RASEVFAGGRYPPEMVAANCISODLSWSKPAQKWEGLLEEVYVYKGG-----VATAK 518
Db 545 KRAIKVVGTPAYEEMVRNQNQLSWKGFKNWENVL--LGLGVAGSAPGIEGDEIAPLA 602
QY 519 KEIKVP 525
Db 603 KENVAAP 609

```

RESULT 7

```

YUBHY
glycogen(starch) synthase (EC 2.4.1.11) precursor - barley
N;Alternate names: starch synthase
C;Species: Hordeum vulgare (barley)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 02-Aug-2002
C;Accession: S01727; S01728
R;Rohde, W.; Becker, D.; Salamini, F.
Nucleic Acids Res. 16, 7185-7186, 1988
A;Title: Structural analysis of the waxy locus from Hordeum vulgare.
A;Reference number: S01727; MUID:88303345; PMID:2970062
A;Accession: S01727
A;Molecule type: DNA
A;Residues: 1-603 <ROH>
A;Cross-references: EMBL:X07931; NID:g19126; PIDN:CAA30755.1; PID:g295809
A;Accession: S01728
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-603 <ROH2>
A;Cross-references: EMBL:X07932; NID:g19128; PIDN:CAA30756.1; PID:g19129
C;Genetics:
A;Gene: waxy
A;Introns: 106/3; 133/3; 166/3; 218/1; 251/3; 369/3; 429/3; 522/3; 565/3
C;Function:
A;Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose producing
A;Pathway: starch biosynthesis
A;Superfamily: starch synthase
C;Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltra

```


QY	2	LDIWMVAEAVAPSKTGGGLGVDVGGGLPIELVKGCHRVMTAPRYDQYADAWDTSVVVDI-	60
Db	82	MNVVYGAENAAPSKTGGGLGVDVGGGLPPAMAANGHVMVSPRYDQYKADMTSVSEIK	141
QY	61	MG---EKRVYFHSIKKGVHRVMDHPWFLAKYMGKTGSKLYGPRSGADYLDNHRKRALFC	117
Db	142	MGDGYEIVRFHCYKRGVDVFDHPLFLERVWGKTEEKIYGGDAGTDYKDNQLRSLLC	201
QY	118	KAATEARVL-----PF--GP-GECDVYVANDWHSALVPVLLKDEYQPKQGTAKASVLA	169
Db	202	QAALEAPRILSLNNPNYFSGPYGEDVYVVCNDWHTGPLSCYLKSNYQSNGIYKDAKTAFC	261
QY	170	IHNATOGRMWEBAFKDTKLPOAAFDKLAFSDCGYAKVYTEATPWEDEXPPLTGKTYKKI	229
Db	262	IHNLSYOGRFASFDFELNLPERKSFDFIDGYE-----PVBE-----RKI	304
QY	230	NWLKGGITAADKLVTSVPNYATIAADAAGVGELDVIRAKGTIEGVNGMDIEWENPKTD	289
Db	305	NWMAKGTLEADRVLTSPYYAEELISGLARGCELDNIMRLTGTITGVNGMDVSEWDPSKD	364
QY	290	KFLSAYDQNSVYAGKAAAKEALQAEGLPVDPTAPLFAFIGRLEROKGVDDIILAALPKI	349
Db	365	KYTAVDYDVSVAEKALNKEALQAEVGLPEVDRKIPLVAFIIGLEEQKQPDVMAAIP-L	423
QY	350	LATPKYQIALITGKAAEYKLVNAIGTKYKGRAGVYKFSAPLAHMLTAGADEMLVPSRF	409
Db	424	LMEEDIQVLVLTGTKKKFERMLSAEKEYDKYRAVVKFNAALAHHIMAGADLLATYSRF	483
QY	410	EPGGLIQLHAMHYGTVPPVVAOSTGGLVDVTVEGVTFGHMGALNDP--KLDEADADALAATV	467
Db	484	EPGGLIQLQMGMYGTCPACASTGGLVDITIEGKTGFHMGRLSDCNWVFADYKKVATTI	543
QY	468	RRASEVFAGGRYEPWVANCISODLSKSPAQKEGLEE---VYVYKGG-----VATAKKE	520
Db	544	KRAIKVGTPTAYEMVKNCMIQDLSNKGPAKNWENVLLSLGVAGGPGTIEGEIAPLAKE	603
QY	521	EIKVP 525	
Db	604	NVAAP 608	

RESULT 11

S07314

glycogen(starch) synthase (EC 2.4.1.11) precursor - maize
N:Alternate names: starch synthase; UDP-glucose starch glycosyltransferase, starch synthase
C:Species: Zea mays (maize)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 02-Aug-2002
C:Accession: S07314
R:Kloessen, R.B.; Gierl, A.; Schwarz-Sommer, Z.; Saedler, H.
Mol. Gen. Genet. 203, 237-244, 1986
A:Title: Molecular analysis of the waxy locus of Zea mays.
A:Reference number: S07314
A:Accession: S07314
A:Molecule type: DNA
A:Residues: 1-605 <KLO>
A:Cross-references: EMBL:X03935; NID:G22509; PTDN:CAA27574.1; PID:gl644339
A:Experimental source: line C
A:Note: Translation of the nucleotide sequence is not complete
A:Note: part of this sequence, including the amino end of the mature protein, was
C:Genetics:
A:Gene: waxy
A:Introns: 107/3; 134/3; 167/3; 197/3; 219/1; 252/3; 289/2; 370/3; 431/3; 495/3
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose pro
C:Superfamily: starch synthase
C:Keywords: amyloplast; chloroplast; glycogen;starch biosynthesis; glycosyltrans
F:1-72/Domain: transit peptide (amyloplast) #status predicted <NP>
F:73-605/Product: glycogen (starch) synthase #status experimental <MAT>

Query Match 40.2% Score 1353.5; DB 1; Length 605;
Best Local Similarity 50.4%; Pred. No. 2e-73;
Matches 275; Conservative 79; Mismatches 153; Indels 39; Gaps 11;

Db 588 ---LUTLKLAI-----GTYTEHKSSWEGLMRRGMDYSDWENAAIQYE 627

RESULT 14

starch synthase (EC 2.4.1.21) precursor - rice
 N:Alternate names: starch synthase
 C:Species: Oryza sativa (rice)
 C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 16-Aug-2002
 C:Accession: JQ2322; PQ0811
 R:Baba, T.; Nishihara, M.; Mizuno, K.; Kawasaki, T.; Shimada, H.; Kobayashi, E.; Ohnishi
 Plant Physiol. 103, 565-573, 1993
 A:Title: Identification, cDNA cloning, and gene expression of soluble starch synthase in
 A:Reference number: JQ2322; MUID:94302151; PMID:7518089
 A:Accession: JQ2322

A:Molecule type: mRNA
 A:Residues: 1-626 <BAB1>
 A:Cross-references: DBJ:16202; NID:9450484; PIDN:BAA03739.1; PID:9450485
 A:Accession: PQ0811
 A:Molecule type: protein
 A:Residues: 114-129 <BAB2>
 A:Experimental source: seed
 C:Function:

A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing e
 C:Superfamily: starch synthase
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
 F:1-113/Domain: transit peptide (amyloplast) #status predicted <TRS>
 F:114-626/Product: ADPglucose-starch glucosyltransferase, 57KD form #status experimental
 F:122-626/Product: ADPglucose-starch glucosyltransferase, 55KD form #status experimental
 F:440-448/Region: substrate binding #status predicted

Query Match 25.9%; Score 873.5; DB 2; Length 626;
 Best Local Similarity 41.5%; Pred. No. 1.1e-44;
 Matches 197; Conservative 77; Mismatches 154; Indels 47; Gaps 13;

QY 4 IVVAAEAVPWSKTGGLDVTGGLPIELVKRHRVMTIAPRY-----DOYADWDTSV 57

Db 135 VVFTGEASPYAKSGGLGDCVGLPTALALRGHRVWVMPRYMNGALNKNFANAFYTEKH 194

QY 58 VDTM---GE-KVRYHSIKGVHRVWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNKR 113

Db 195 IKIPCGGHEVTFEYRSDVDWVFWDFPSY-----HRPNLYGDNFCA-FGDNQF 247

QY 114 ALFCKAAIEAARVLPGP---GEDCVFVANDHISALVPVLLKDEYQPKGFTAKSVLA 170

Db 248 TLCLYACAEAPLLELGGYTYGQKCMFVNDHWSALVPLLAARYPYGVYRDARSVLVI 307

QY 171 HNIAGQRMWEAEAFKDTKLPOAAFDKLAISDGYAKVYVTEATPMEDEKPLTGKTKIN 230

Db 308 HNLHOGVEPASTYDGLPPEWYGALW-----VPEWARHLDKG-----EAVN 354

QY 231 WLKGGIIADKLVTSNPTATEIAAAGGVLDTVI--RAKGIEGIVNGMDIEEWNPK 288

Db 355 FLKGVVTAADRVITVSQGSWEVTT-AEGGGLNELLSRKSVLNGIVNGIDINDNPST 413

QY 289 DKFLSAPYDQNSVYAKAAKALQALQELGLPVDPTAPLFAFGRLEEQKGVDTILALPK 348

Db 414 DKFLPYHSVDL-SGAKCKAEQLQELGLPIRPDVLPIGFLIGRLDYQKGLIKLAIPD 472

QY 349 ILATPKVQIATLGTKAAVEKLVNAIGTKYKRAKGVVVFSAPLAHMLTAGADFMVPSR 408

Db 473 LM-RDNIQVLMGSDGDFEGHWRSTESYRKFRGWGFSVPVSHRITAGDILMPSR 531

QY 409 FPECGLIQLHAMHYGTVPVVASTGGLVDTVK-----EGVTGFHMGALNPK 454

Db 532 FPECGLNQLYAMQYGVTPVWVHGTGLRDTVENFNFPAEKGEQGTGWAFFLIEK 586

RESULT 15

T01208

starch synthase (EC 2.4.1.21) isoform STSII-1 - maize (fragment)

N:Alternate names: starch synthase isoform STSII-1

C:Species: Zea mays (maize)
 C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Aug-2002
 C:Accession: T01208
 R:Knight, M.E.; Harn, C.; Lilley, C.E.R.; Guan, H.P.; Singletary, G.W.; Mu-Forester,
 Plant J. 14, 613-622, 1998
 A:Title: Molecular cloning of starch synthase I from maize (W64A) endosperm and expr
 A:Reference number: Z14279; MUID:98340555; PMID:9675904
 A:Accession: T01208

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-732 <KN1>
 A:Cross-references: EMBL:AF019296; NID:92811133; PIDN:AAD13341.1; PID:g2655029
 A:Experimental source: strain W64A; endosperm
 C:Genetics:
 A:Gene: SSIIa
 C:Function:

A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose produci
 C:Superfamily: starch synthase
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 25.9%; Score 872; DB 2; Length 732;
 Best Local Similarity 39.7%; Pred. No. 1.7e-44;
 Matches 211; Conservative 77; Mismatches 178; Indels 66; Gaps 15;

QY 2 LDIVAAEAVPWSKTGGLDVTGGLPIELVKRHRVMTIAPRYDQYADWDTSV--VVD 59

Db 241 MNVIVAAECPWCKTGGGLDVTGGLPKALARRHRVWVVPVRYGDIYVEAFDMGIRKYYK 300

QY 60 IMGE--KVRYHSIKGVHRVWIDHPWFLAK---VWGKTGSKLYGPRSGADYLDNKRKFA 114

Db 301 AAGQDLEVNFHAFIDGVDFIDAPLFRHQDDIYGSRQFIM-----KRM 348

QY 115 LFCKAAIEAARVLP-----FGEDCVFVANDHISALVPVLLKDEYQPKGFTAKSVLA 169

Db 349 LFCKAVAEVPHVPCGGVCGYGDG-NLAFIANDHWTALLPYLYKAYYRDHGLMQYTRSLV 407

QY 170 IHNIAFGQRMWEAEAFKDTKLPOAAFDKLAISDGYAKVYVTEATPMEDEKPLTGKTKYKI 229

Db 408 IHNIAHOGRGVDFEFPYMDLPEHYLQHFELD-----PVGG---EHA 446

QY 230 NLKGGIIADKLVTSNPTATEIAAAGGVLDTVIRAKG--IEGIVNGMDIEEWNPK 287

Db 447 NIFAAGLKMDRVVTVSRGYLWELKT-VEGGWGLHDIIRSNWDKINGIVNGIDHGEWNP 505

QY 288 TDKFLSAP---YDQNSVYAKAAKALQALQELGLPVDPTAPLFAFGRLEEQKGVDTIL 343

Db 506 VDHLRSDGYTNSLETLDAGKCKOAKALQELGLEVRDVPVPLGFLIGRLDGKGVDTIG 565

QY 344 AALPKIATPKVQIATLGTKAAVEKLVNAIGTKYKRAKGVVVFSAPLAHMLTAGADFM 403

Db 566 DAMPWI-AGODVQLVMLGTGRADIERMLQHLREHPNKGWVGFSVPMARITAGADVL 624

QY 404 LVPSREPCGLIQLHAMHYGTVPVVASTGGLVDTVKE---GVTFGHMGALNPKDLDEAD 459

Db 625 VMSREPEPCGLNQLYAMQYGVTPVWVHGTGLRDTVAFDFPDGAGLW-----TFDRAE 678

QY 460 ADALAAVTRRASVEA--GGRYPEMVAANCISQDLSWSKPAQKREGGLEVVVY 509

Db 679 ANKLIEALRHCLDTYRKYGESWKSQARGMSQDLSWDHAAELYEDVLVAKY 730

Search completed: June 4, 2003, 14:57:31
 Job time : 21.8268 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 13:50:41 ; Search time 8.74119 Seconds
(without alignments)
3088.950 Million cell updates/sec

Title: US-09-980-771a-5

Perfect score: 3370

Sequence: 1 ALDINVAAAEVAPWSKTGL.....SASKTAAKPLVSAATRKSA 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1481.5	44.0	608	1 UGST_MANES	Q43784 manihot esc
2	1457.5	43.2	607	1 UGST_SOLTU	Q00775 manihot tub
3	1455.5	43.2	608	1 UGST_ANTMA	O82627 antirrhinum
4	1415.5	42.0	603	1 UGST_PEA	Q43092 pisum sativ
5	1412.5	41.9	608	1 UGST_IPOBA	Q42857 ipomoea bat
6	1397.5	41.5	609	1 UGST_ORYSA	P19395 oryza sativ
7	1395.5	41.4	603	1 UGST_HORVU	P09842 hordeum vul
8	1394.5	41.4	609	1 UGST_ORYGL	Q42968 oryza glabe
9	1362	40.4	615	1 UGST_WHEAT	P27736 triticum ae
10	1355.5	40.2	608	1 UGST_SORBI	Q43134 sorghum bic
11	1353.5	40.2	605	1 UGST_MAIZE	P04713 zea mays (m
12	902.5	26.8	641	1 UGST_SOLTU	P93568 solanum tub
13	873.5	25.9	626	1 UGST_ORYSA	Q40739 oryza sativ
14	871	25.8	752	1 UGST_PEA	Q43093 pisum sativ
15	869	25.8	610	1 UGST_WHEAT	Q43654 triticum ae
16	847.5	25.1	788	1 UGST_SOLTU	Q43847 solanum tub
17	684.5	20.3	477	1 GLG3_STRPN	Q97qs5 streptococc
18	677.5	20.1	484	1 GLGA_BACSU	P39125 bacillus su
19	670.5	19.9	485	1 GLGA_BACST	O08328 bacillus st
20	669	19.9	478	1 GLGA_LACLA	Q9chm9 lactococcus
21	653.5	19.4	480	1 GLGL_RHIME	P58393 rhizobium m
22	652	19.3	480	1 GLGA_AGRST5	P39670 agrobacteri
23	651	19.3	486	1 GLGA_THEMEA	Q9wz27 thermotoga
24	646.5	19.2	480	1 GLGA_RHITR	Q9euts rhizobium t
25	637	18.9	477	1 GLGA_CLOAB	Q97cx6 clostridium
26	622	18.5	482	1 GLGA_CLOPE	O8xpa1 clostridium
27	622	18.5	484	1 GLGA_VIBCH	Q9kdb6 vibrio chol
28	614.5	18.2	476	1 GLGA_BACHD	Q9kdx6 bacillus ha
29	604.5	17.9	486	1 GLG2_RHIME	P58394 rhizobium m
30	604	17.9	476	1 GLGA_YERPE	O8za78 yersinia pe
31	602.5	17.9	481	1 GLGA_RHULO	Q985p2 rhizobium l
32	587	17.4	477	1 GLGA_ECOLI	P08323 escherichia
33	587	17.4	477	1 GLGA_SALTU	Q8z232 salmonella

34 580 17.2 477 1 GLGA_SALTU
35 578 17.2 480 1 GLGA_PASMU
36 569 16.9 476 1 GLGA_HAEIN
37 568.5 16.9 1230 1 UGST_SOLTU
38 560.5 16.6 472 1 GLGA_ANASP
39 555 16.5 461 1 GLGA_FUSNN
40 552.5 16.4 463 1 GLGA_AQUAE
41 538 16.0 465 1 GLGA_SYNP7
42 536 15.9 477 1 GLGA_RHOSH
43 536 15.9 492 1 GLG2_ANASP
44 535 15.9 477 1 GLGA_SYNP3
45 527 15.6 444 1 GLGA_DEIRA

ALIGNMENTS

RESULT 1

UGST_MANES STANDARD; PRT; 608 AA.
AC Q43784;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
GN WAXY OR GBSS.
OS Manihot esculenta (Cassava) (Manioc).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Manihot.
OX NCBI_TaxID=3983;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. M.COL 22; TISSUE=Tuberos root;
RX MEDLINE=94083565; PubMed=8260633;
RA Salehuzzaman S.N., Jacobsen E., Visser R.G.F.;
RT "Isolation and characterization of a cDNA encoding granule-bound
starch synthase in cassava (Manihot esculenta Crantz) and its
antisense expression in potato."
RL Plant Mol. Biol. 23:947-962(1993).
CC -!- FUNCTION: RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE IN RESERVE
STARCH
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- TISSUE SPECIFICITY: SYNTHESIZED IN A NUMBER OF DIFFERENT ORGANS,
BUT MOST ABUNDANTLY IN TUBERS.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL: X74160; CAA52273.1; -
DR InterPro: IPR001296; Glycos.transf_1.
DR Pfam: PF00534; Glycos.transf_1; 1.
KW Glycogen biosynthesis; transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Starch biosynthesis.
FT TRANSIT 1 78 CHLOROPLAST [BY SIMILARITY].
FT CHAIN 79 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT BLINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 608 AA; 68968 MW; C9C970CD3011BDBB CRC64;

Query Match 44.0%; Score 1481.5; DB 1; Length 608;
Best Local Similarity 55.0%; Pred. No. 2.4e-81;
Matches 299; Conservative 64; Mismatches 148; Indels 33; Gaps 9;

Qy	2	LDIVMAAEVAPSWSTGGIGDVTGGPLTELVKRGHRVMTIAPRYDOYADAWDTISVVVDI-	60
Db		:::	
Qy	82	NMLIFVGAEVGWSKTGGIGDVLGGIPMAARGHRVMTVSPRYDOYKAWDTISVSVEIK	141
Db			
Qy	61	MG---EKVRYSHSTIKKGVRHVWIDHPWFLAKYWGKTSLKYGTPRSGADYLDNHHKRALFC	117
Db		:	
Qy	142	IGDRIETVRFPHSYKRGVDRVDFVDPHMLEKVMGKTSGKIYGPRAGLDYQDNQLRSLLC	201
Db		:	
Qy	118	KAATEAARVLFF-----GP-GEUCVAVANDWHSALVPVLKDEYQPGQFTKAKSVLA	169
Db		:	
Qy	202	LAALAPRVNLNLSKNFSGPYGEVAFIANDWHTALTFCYLKAIYPMGIYKHAKVAFC	261
Db		:	
Qy	170	IHNIAFOGRMWEEAFKDTKLPOAADFKLAFSDGYAKVYTEATPMEEDEKPLTKGYTKI	229
Db		:	
Qy	262	IHNIAYGGRFAFSDFPRLNLPDKFKSSDFIDGYEK-----PVKG---RKI	304
Db		:	
Qy	230	NWLKGGIIAADKLVTVSPNYATEIADAAGGVELDTVIRAKGIEGVNGMDTEENPKTD	289
Db		:	
Qy	305	NWMKAGLLESDRVLTVSPYQAQVTSYGVERGVVELDNTRKTGIAGIINGMDVQWENPVD	364
Db		:	
Qy	290	KFLSAPYDONSIVYAGKAAAKALQALGLPVDPTAPLFAFGRLEBQGVDIILALPKI	349
Db		:	
Qy	365	KYDIDHDTATYMDAKPLLKALQAEVLVDNRNVLPTGFTGRLEBQGSDFVAAISO-	423
Db		:	
Qy	350	LATPKVQIALGTGKAAYEKLVINAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVLPSRF	409
Db		:	
Qy	424	IVENHVQIVILGTGKKKFKQIEHLEVLVYDPKARGVAKFNVLPHMIIITAGADFMVLPSRF	483
Db		:	
Qy	410	EPCLLIQLHAMHGTVPVAVASTGGLVDTVKESVTGFHMGALNP--DKLEADADALAATV	467
Db		:	
Qy	484	EPCLLIQLHAMRYGTVPVIVASTGGLVDTVKESVTGFQMGALHVECCDKIDSADVAIVKTV	543
Db		:	
Qy	468	IRASEVFAAGRYPEMWANGSITSDLSWSKPAQKWESGLLEEYVYGKGVATAKKEEIKVPVA	527
Db		:	
Qy	544	ARALGYATAALREMILNCAQDLWSKGPARNWEKMLDLLEV-TGSEFGTGEETAPLAK	602
Db		:	
Qy	528	EKTP	531
Db		:	
Qy	603	ENVP	606
Db		:	

RESULT 2

UGST_SOLTU	STANDARD;	PRT;	607 AA.
ID	UGST_SOLTU		
AC	Q00775;	Q43176;	
DT	01-APR-1993	(Rel. 25, Created)	
DT	01-APR-1993	(Rel. 25, Last sequence update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	
DE	Granule-bound glycogen [starch] synthase, chloroplast precursor		
DE	(EC 2.4.1.11).		
GN	WAXY OR GBSS.		
OS	Solanum tuberosum (Potato).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
OX	NCBI_TaxID=4113;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RC	STRAIN=AM79.7322;		
RX	MEDLINE=91360072; PubMed=18866009;		
RA	van der Leij F.R., Visser R.G.F., Ponstein A.S., Jacobsen E.,		
RA	Feenstra W.J.;		
RT	"Sequence of the structural gene for granule-bound starch synthase of		
RT	potato (<i>Solanum tuberosum</i> L.) and evidence for a single point		
RT	deletion in the amf allele."		
RL	Mol. Gen. Genet. 228:240-248(1991).		
RL	[2]		
RP	REVISONS.		
RA	van der Leij F.R.;		
RL	Submitted (JUN 1992) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		

```

CC STRAIN=cv. Dongnong 303;
CC Dai W.L., Deng W., Cui M., Xiu M., Zhao S.Y., Wang X.M.;
CC RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + [(1,4)-alpha-D-glucosyl](N) =
CC UDP + [(1,4)-alpha-D-glucosyl](N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X58453; CAA41359.1; -
CC EMBL; X83220; CAA58220.1; -
CC PIR; SL6555; YUPOY.
CC InterPro: IPR001296; Glycos_transf_1.
CC Pfam; PF00534; Glycos_transf_1.
CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
CC Transit peptide; Chloroplast; Starch biosynthesis.
CC TRANSIT 1 77
CC CHLOROPLAST.
CC CHAIN 78 607
CC BINDING 95 95
CC CONFLICT 130 130
CC CONFLICT 398 398
CC SEQUENCE 607 AA; 66575 MW; 2A377865CFFA650 CRC64;
CC -----
CC [STARCH] SYNTHASE.
CC UDP-GLUCOSE (BY SIMILARITY).
CC A -> T (IN REF. 3).
CC I -> V (IN REF. 3).
CC -----

```

Query Match

QY	2	LDIVMAAEAVP	SKTGGLG	DVGTGGL	PIELV	KGRHVMT	IAPRYDQ	ADAWDT	SVVVDI	60
Db	81	MNLI	VTEGVP	SKTGGLG	DVLGGLP	ALAAARGH	YMTISPR	YDQTKD	AWDTSA	VEV
QY	61	MG---	EKVRYF	SHSTK	GVHVR	WDHP	WFLAK	VNGK	SGKLYG	PPSGADYLDN
Db	141	VGDS	IELVRE	FHCYK	RGVDR	VFVDH	PMFLK	VNGK	SGKLYG	KAGLDYLDN
QY	118	KA	IEAAR	VL	LPF-----	GP	-GDCV	FVAND	HSALV	PPVLLK
Db	201	QA	AEAPK	VNLN	SSNV	FGSP	YGED	VLF	IAND	WHTAL
QY	170	IHN	IAFG	RWE	EAF	KD	TKLPQ	AAFK	KLAF	SDG
Db	261	IHN	IAFG	R	W	EAF	KD	TKLPQ	AAFK	KLAF
QY	230	NML	KG	IIA	D	L	V	T	S	P
Db	304	NM	KAGIL	SH	R	V	T	S	P	Y
QY	290	K	LSA	P	Y	D	Q	N	S	V
Db	364	K	Y	D	Q	N	S	V	Y	A
QY	350	L	A	T	P	K	V	Q	I	A
Db	424	I	G	L	-	D	V	Q	I	A
QY	410	E	P	C	G	L	I	Q	L	H
Db	483	E	P	C	G	L	I	Q	L	H
QY	458	P	R	A	S	V	F	A	G	G
Db	543	A	R	A	L	A	V	G	T	L
QY	520	B	E	I	K	V	P	525		

[illegible]

RESULT 6
UGST_ORYSA
ID UGST_ORYSA STANDARD; PRT; 609 AA.
AC P19395; Q43013;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
DE WAXY OR WX.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=92322986; PubMed=1377969;
RA Okagaki R.J.;
RL "Nucleotide sequence of a long cDNA from the rice waxy gene.";
RN Plant Mol. Biol. 19:513-516(1992).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica Taichung 65; TISSUE=Seedling;
RA Hirano H.Y., Sano Y.;
RL "Molecular characterization of the waxy locus of rice (Oryza
sativa).";
RN Plant Cell Physiol. 32:989-997(1991).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica, and cv. Hanfeng;
RX MEDLINE=91016948; PubMed=2216792;
RA Wang Z.Y., Wu Z.L., Xing Y.Y., Zheng F.G., Guo X.L., Zhang W.G.,
RA Hong M.M.;
RL "Nucleotide sequence of rice waxy gene.";
RN Nucleic Acids Res. 18:5898-5898(1990).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Indica;
RA Wang X.Q., Wang Z.Y., Hong M.M.;
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE OF 153-343 FROM N.A.
RX MEDLINE=91200672; PubMed=2016064;
RA Shimada H., Tada Y.;
RL "Rapid isolation of a rice waxy sequence: a simple PCR method for the
analysis of recombinant plasmids from intact Escherichia coli
cells.";
RN Gene 98:243-248(1991).
RC -!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + [(1,4)-alpha-D-glucosyl](N) =
CC UDP + [(1,4)-alpha-D-glucosyl](N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X62134; CAA44065.1; -
DR EMBL; X58228; CAA41186.1; -
DR EMBL; X53694; CAA37732.1; -
DR EMBL; X65183; CAA46294.1; -
DR EMBL; M55039; AAA33918.1; -
DR PIR; JQ0703; JQ0703.
DR PIR; S22519; S22519.

```

OX RN NCBI_TaxID=4513;
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Vogelsanger Gold; TISSUE=Leaf;
RX MEDLINE=88303345; PubMed=2970062;
RA Rhode W., Becker D., Salamini F.;
RT "Structural analysis of the waxy locus from Hordeum vulgare.";
RL Nucleic Acids Res. 16:7185-7186(1988).
RN [2]
RP SEQUENCE OF 76-89.
RC STRAIN=cv. H354-295-2-5; TISSUE=Starchy endosperm;
RX MEDLINE=94170739; PubMed=8125056;
RA Flensburg R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional electrophoresis.";
RL Electrophoresis 14:1060-1066(1993).
CC -!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) -
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X07931; CAA30755.1; -.
CC EMBL: X07932; CAA30756.1; -.
CC PIR: S01727; YUBHY.
CC InterPro: IPR001296; Glycos_transf_1.
CC Pfam: PF00534; Glycos_transf_1; 1.
CC GlycoGen biosynthesis; Transferase; Glycosyltransferase;
CC Transit peptide; Chloroplast; Starch biosynthesis.
CC TRANSIT 1 72 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 73 603 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
CC BINDING 90 90 UDP-GLUCOSE (BY SIMILARITY).
CC SEQUENCE 603 AA; 66211 MW; 0B0B3DE6A8217934 CRC64;
CC
CC Query Match 41.4%; Score 1395.5; DB 1; Length 603;
CC Best Local Similarity 53.3%; Pred. No. 3.3e-76;
CC Matches 277; Conservative 71; Mismatches 141; Indels 31; Gaps 7;
QY 2 LDIVMVAEAPWPKSGGLGDLVGGTGLPIELVKRGHRVMTIAPRYDOYADAWDTSVVVDIM 61
DB 76 MNLVFGAEMAPWPKSGGLGDLVGGTGLPIELVKRGHRVMTIAPRYDOYADAWDTSVVVDIM 135
QY 62 ----GEKVRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSGLYGRSGADYLDNHRKRALFC 117
DB 136 VADEYERVRFFHCYKRGVDRVFDHPWFLAKVWGKTSGLYGRSGADYLDNHRKRALFC 195
QY 118 KAAIEARVL----PF--CP-GEDEVFANDHWSALVPVLLKDEYQPGQFTKASVLA 169
DB 196 QALAEAPRLNLNNDYFGSGPYGDEVFVFCNDWHDTGLLACYLKSNTQSGIYRTAKVAF 255
QY 170 IHNIAFGQRMWEAEFKDTLPQAAFDKLAFCSDYAKVYVTEATPMEDEKPLTGKTKYKI 229
DB 256 IHNISVQGRSFDDFAQLNLPDRFKSFFDFIDYDK-----PVEG-----RKI 298
QY 230 NMLKGIITAAKLVTVSPNYATEIADAAGGVVELDTVIRAKGIEGIVNGMDIEWNPKTD 289
DB 299 NNMKAGILQADVLAVSPYIAEELISGEARGCELDNIMRLTGTITGVNMDVSEWDPTKD 358
QY 290 KFLSAPYDQNSYAGKAAKAEALQALGLPVPDTPAPLFAFIGNLEQKGVLDIILALPKI 349
DB 359 KFLAVNYDITTALEKALNKEALQAEVGLPVDKRPVLAFIGRLEEQKGPDMYIAIPEI 418
QY 350 LATPKVQIAILGTGKAAAEKLVNAICTKYKGRAGKGVKFPAPLAHMLTAGADFMVLVPSRF 409

```

```

DB 419 LKEEDVQIILLGTGKKKEKLKSMEEKPPGKVRVAVRENAPLAHOMAGADLLAVTSRF 478
QY 410 EPCGLLIQIHAMHYGTVFVAVSTGGVLDIVKGVTFHMGALNPD--KIDEDADALAAATV 467
DB 479 EPCGLLIQIOMGRYGTGTCVASTGGVLDIVKGVTFHMGALNPD--KIDEDADALAAATV 538
QY 468 KRASEVFAGGRYPVEMVANCISQDLSWSPKPAOKWEGLEEV 507
DB 539 KRKYVGVTFPAYQEMVKNMIOQLSWKGPARNWEDVLEL 578
RESULT 8
ID UGST_ORYGL STANDARD; PRT; 609 AA.
AC 042968;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor (EC 2.4.1.11).
DE GN WAXY.
OS Oryza glaberrima (African rice).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC Ehrhartoideae; Oryzeae; Oryza.
CC NCBI_TaxID=4538;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. GMS1;
CC MEDLINE=92134825; PubMed=1685658;
CC Umeda M., Ohtsubo H., Ohtsubo E.;
CC "Diversification of the rice Waxy gene by insertion of mobile DNA elements into introns.";
CC Jpn. J. Genet. 66:569-586(1991).
CC -!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) -
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D10472; BAA01272.1; -.
CC InterPro: IPR001296; Glycos_transf_1.
CC Pfam: PF00534; Glycos_transf_1; 1.
CC GlycoGen biosynthesis; Transferase; Glycosyltransferase;
CC Transit peptide; Chloroplast; Starch biosynthesis.
CC TRANSIT 1 77 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 78 609 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
CC BINDING 97 97 UDP-GLUCOSE (BY SIMILARITY).
CC SEQUENCE 609 AA; 66475 MW; C228BFB9C407FA5 CRC64;
CC
CC Query Match 41.4%; Score 1394.5; DB 1; Length 609;
CC Best Local Similarity 51.4%; Pred. No. 3.8e-76;
CC Matches 281; Conservative 75; Mismatches 148; Indels 43; Gaps 9;
QY 2 LDIVMVAEAPWPKSGGLGDLVGGTGLPIELVKRGHRVMTIAPRYDOYADAWDTSVVVDI- 60
DB 83 MNLVFGAEMAPWPKSGGLGDLVGGTGLPIELVKRGHRVMTIAPRYDOYADAWDTSVVVDI- 142
QY 61 ----MEKVRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSGLYGRSGADYLDNHRKRALFC 117
DB 143 VADRYERVRFFHCYKRGVDRVFDHPWFLAKVWGKTSGLYGRSGADYLDNHRKRALFC 202

```



```

[1]
SEQUENCE FROM N.A.
RC STRAIN=cv. 12311; TISSUE=Seed;
RA Hsing Y.C., Liu C., Yu H., Hsieh J.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
CC -|- PATHWAY: Starch biosynthesis.
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U23945; AAC49804.1; -.
CC InterPro: IPR001296; Glycos_transf_1.
CC Pfam: PF00534; Glycos_transf_1; 1.
CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
CC Transit peptide; Chloroplast; Starch biosynthesis.
CC TRANSIT 1 77 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 78 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
CC BINDING 97 97 UDP-GLUCOSE (BY SIMILARITY).
CC SEQUENCE 608 AA; 66074 MW; C31333FA87D2D8A6 CRC64;
CC -----
Query Match 40.2%; Score 1355.5; DB 1; Length 608;
Best Local Similarity 50.6%; Pred. No. 8.2e-74;
Matches 276; Conservative 76; Mismatches 154; Indels 39; Gaps 11;
QY 2 LDIIVMAAEVAPWSKTGGLDVTGGLPIELVKRHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82 MNVVFVGAEMAPWSKTGGLDVLGGLPPAMAANGHRVWVSPRYDQYKAWDTSVYSEIK 141
QY 61 MG---EKVYFHSIKKGVHRVWIDHPFLAKVWGKTSGLYKPRSGADYLDNHRKRALFC 117
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
142 MGDGYETVRFFHCYKRGVDRVFDHPLFLERVWGKTEEKIYGPDAITGDKNQLRFSLLC 201
QY 118 KAAIEARVLI-----PF--GP-GEDEVFVANDHWSALVPVLLKDEYQPKGQFTAKSVLA 169
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
202 QAALEAPRILSLNNNPFSGPYGDEVVFCNDWHITGPLSCYLSKNSYQSNGIYKDAFTAF 261
QY 170 IHNIAFQGRWEEAFKDTKLPOAFAFDKLAFCSDGYAKVYTEATPMEDEKPPLTGKYKKI 229
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
262 IHNISYQGRFATSDPELNLPERFKSSDFIDGYEK-----PVGE---RKI 304
QY 230 NWLKGILIAADKLIVTSPNYATEIAADAAGGVLDIVIRAKGIEGIVNGMDIEWNPXTD 289
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
305 NNMKAGILEADRLVIVSPYAEELISGIARGCELDNIMRLTGITGVNGMDVSEWDPKSD 364
QY 290 KFLSAPYDQNSVYAGKAAKALQAEGLPVPDPTAPLEAFIGRLEQKGVDDIILALPKI 349
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
365 KYIAVKYDVSTAVEAKALNKEALQAEVGLPVDKIKPLVAFIGRLEQKGVDPVMAAIP-L 423
QY 350 LATPKVQIATLGTAKEKLVNAICTYKGRAGVVKFSAPLAHMLTAGADFMVLPSPRF 409
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
424 LMEEDIQVLLGTGKKPERMLMSAEKYPDKRVAVKFNENALAHHIMAGADLLAVTSRF 483
QY 410 EPCGLIQLHAMHYGVVPVASTGGLVDTVVKEGVTGFHGMALNPD--KLDEADADALAAIV 467
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
484 EPCGLIQLQGMRYGTPPCASTGGGLVDITIEGKTGFHMGRLSVDCNVCVBPADVKKVATL 543
QY 468 RRASEVFAGGRYPENVANCISODLSWSPKPAQKWEGLLEE--VYKGG-----VATAKE 520
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
544 KEALIKVGTPTAEEVMKNCMIQDLSWKGPAKNWENVLISLVAGGEPGIEGEIAPLAKE 603
QY 521 ELKVP 525
Db 604 NVAAP 608

```

```

RESULT 11
UGST_MAIZE STANDARD; PRT; 605 AA.
AC PG04713;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
GN WAXY.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Koesgen R.B., Gierl A., Schwarz-Sommer Z., Saedler H.;
RT "Molecular analysis of the waxy locus of Zea mays.";
RL Mol. Gen. Genet. 203:237-244(1986)
CC -|- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
CC -|- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
CC -|- PATHWAY: Starch biosynthesis.
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND
CC -|- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC -----

```

```

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@isb-sib.ch).

```

```

EMBL: X03935; CAA27574.1; -.
EMBL: M24258; AAA33520.1; -.
PIR: S07314; S07314.
MaizeDB; 15806; -.
InterPro: IPR001296; Glycos_transf_1.
Pfam: PF00534; Glycos_transf_1; 1.
Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Starch biosynthesis.
FT TRANSIT 1 72 CHLOROPLAST.
FT CHAIN 73 605 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 91 91 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 605 AA; 65966 MW; 137F15207DBFC189 CRC64;

```

```

Query Match 40.2%; Score 1353.5; DB 1; Length 605;
Best Local Similarity 50.4%; Pred. No. 1.1e-73;
Matches 275; Conservative 79; Mismatches 153; Indels 39; Gaps 11;
QY 2 LDIIVMAAEVAPWSKTGGLDVTGGLPIELVKRHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
77 MNVVFVGAEMAPWSKTGGLDVLGGLPPAMAANGHRVWVSPRYDQYKAWDTSVYSEIK 136
QY 61 MG---EKVYFHSIKKGVHRVWIDHPFLAKVWGKTSGLYKPRSGADYLDNHRKRALFC 117
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
137 MGDGYETVRFFHCYKRGVDRVFDHPLFLERVWGKTEEKIYGVAGTDYDNDQLRFSLLC 196
QY 118 KAAIEARVLI-----PF--GP-GEDEVFVANDHWSALVPVLLKDEYQPKGQFTAKSVLA 169
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
197 QAALEAPRILSLNNNPFSGPYGDEVVFCNDWHITGPLSCYLSKNSYQSNGIYKDAFTAF 256
QY 170 IHNIAFQGRWEEAFKDTKLPOAFAFDKLAFCSDGYAKVYTEATPMEDEKPPLTGKYKKI 229
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 IHNISYQGRFATSDPELNLPERFKSSDFIDGYEK-----PVGE---RKI 299
QY 230 NWLKGILIAADKLIVTSPNYATEIAADAAGGVLDIVIRAKGIEGIVNGMDIEWNPXTD 289
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 300 NWMKAGILEADRVLTSPYABELISGIARGCELDNIMRLTGLTGIVNGMDVSEWDPGRD 359
 QY 290 KFLSAPYDQNSVYAGAAKALQAEGLGVDPDTAPLFAFTGRLEBQKGVDIILALPKI 349
 Db 360 KYIAKYDVSTAVEKALKALQAEVGLPVDRNPLVAFITGRLEBQKGVDPVMAAIPOL 419
 QY 350 L-ATPKVQITAILGTGKAAYEKLVNAGITKYKRAKGVVVKFSAPLAHMTAGADFMVPSR 408
 Db 420 MEMVEDVOITLGTCKKFERMLMSAEKFKPKVRVAVKVFNAALAHIMAGADVLAVTSR 479
 QY 409 FEPGGLIOLHAMHYGTVPVASTGGLVDTVKEGVTCFHMALNPD--KLDEADADALAT 466
 Db 480 FEPGGLIOLQGRYGTCPACASTGGLVDTVIEGKTGFHMGRUSVCNVVPEADVKKVAT 539
 QY 467 VRRASEVAGGYPWVANCISQDLSWSKPAQKWEGLLEE--VYKGGGV-----ATAK 519
 Db 540 LQRAIKVYGTPAYEEMVRNCMTQDLSWKGPAKNWENVLISLVAGEPGVEGEIAPLAK 599
 QY 520 EIKVP 525
 Db 600 ENVAAP 605

RESULT 12

UGS2_SOLU STANDARD; PRT; 641 AA.
 AC P93568;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Soluble glycogen [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11) (SS I).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 ON NCBI_TaxID=4113;
 RX [1]
 SEQUENCE FROM N.A.
 RP STRAIN=cv. Desiree; TISSUE=Leaf;
 RX MEDLINE=97164391; PubMed=9011082;
 RA Abel G.J.W., Springer F., Willmitzer L., Kossmann J.;
 RT "Cloning and functional analysis of a cDNA encoding a novel 139 kDa
 starch synthase from potato (Solanum tuberosum L.).";
 RL Plant J. 10:981-991(1996).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
 UDP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
 SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL; Y10416; CAA71442.1;
 DR InterPro; IPR001296; Glycos_transf_1.
 DR Pfam; pf00534; Glycos_transf_1; 1.
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
 FT TRANSIT ? CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 641 SOLUBLE GLYCOGEN [STARCH] SYNTHASE.
 FT BINDING 145 145 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 641 AA; 70608 MW; 30F8B0546CEFB74C CRC64;

Query Match 26.8%; Score 902.5; DB 1; Length 641;
 Best Local Similarity 39.8%; Pred. No. 9.9e-47;

Matches 212; Conservative 90; Mismatches 161; Indels 69; Gaps 19;
 QY 3 DIVMAAEVAPSKTGGLGDTVGGPFIELVKGRHRYMTIAPRY-----DOYADAWDTS 55
 Db 132 NIIFVTAERAPYSKTGGLGDCVSLPMAAARHVRVWVSPRYLNGSPSDEKYANAVDLD 191
 QY 56 V--VVDIMG--EKVRFHSIKKGVHVWIDHPWFLAKVWGKTGSKLYGSPSGADYLDNHK 111
 Db 192 VRAIVHCFDAQAEVAFYHEYRAGVWVFDHSSYC-----RPGTP--YGDYIGA-FGDNQF 244
 QY 112 REALFCKAIEAARVLPEGP--GDCVFVANDHWSALYVPLIKDEYKPGQFTKAKSVL 168
 Db 245 RFTLLSHAACEAPVLPPLGFGTYGKCLFLANDHAAVPLLLAAKYRPGVGVKDARSIV 304
 QY 169 AIHNTIAFOGRMWEAFKDKLPQAFKLSDSGYAKVYTEATPMEDEKPPITGKYTK 228
 Db 305 AIHNTIAHQGVPAVTYNNLGLPPQWYGAV---EWIETPTWARHALD-----TGET--- 351
 QY 229 INWLKGIITAAADKLVTVSPNYATEIAADAAGGVLEDTVI--RAKGTGIVNGMDIEWNP 286
 Db 352 VNYLKGAIAVADRILTVSOGYSWEIIT-PEGGYLHELHSSROSVLNGTINGIDVNDWNP 410
 QY 287 KTDKLSAPYDQNSVYAGAAKALQAEGLGVDPDTAPLFAFTGRLEBQKGVDIILAL 346
 Db 411 STDEHTASHYSINDL-SGKVQCKTDLQKELGLPIRDPDCLIGFIRGLDYKQGVDIILSAI 469
 QY 347 PKILATPKVOITAILGTGKAAYEKLVNAGITKYKRAKGVVVKFSAPLAHMTAGADFMVLP 406
 Db 470 PELMQN-DVQVVMVLSGSEKQYEDWMRHTENLFKDFRAWVGFNVPVSHRTAGCDIILMP 528
 QY 407 SRPECGLIOLHAMHYGTVPVASTGGLVDTV-----EGV---TGFHMGALNPDKLD 456
 Db 529 SRPECGLNOLYAMRYGTPIPIVHSTGGRLDVFDPNPAQEGEGTGCTWTFSPITSKL- 587
 QY 457 EADADALATVRRASEVFAAGRYPE-----MVANCISQDLSWSKPAQKWE 501
 Db 588 ---LDILKLA-----GTYTEHKSWEGLMRMGGRDYSWENAAIQYE 627
 RESULT 13
 UGS2_ORYSA STANDARD; PRT; 626 AA.
 AC Q40739;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Soluble glycogen [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11) (SSS).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 ON NCBI_TaxID=4530;
 RX [1]
 SEQUENCE FROM N.A. AND SEQUENCE OF 114-131.
 RP STRAIN=cv. Japonica; TISSUE=Seed;
 RX MEDLINE=94302151; PubMed=7518089;
 RA Baba T., Nishihara M., Mizuno K., Kawasaki T., Shimada H.,
 RA Kobayashi E., Ohnishi S., Tanaka K.-I., Arai Y.;
 RT "Identification, cDNA cloning, and gene expression of soluble starch
 synthase in rice (Oryza sativa L.) immature seeds.";
 RL Plant Physiol. 103:565-573(1993).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
 UDP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE.
 CC -1- TISSUE SPECIFICITY: LEAVES AND IMMATURE SEEDS
 CC -1- MISCELLANEOUS: THREE FORMS OF SOLUBLE STARCH SYNTHASE WERE
 CC PURIFIED: RSS1, RSS2 AND RSS3.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:35:26 ; Search time 32.3424 Seconds
(without alignments)
4147.394 Million cell updates/sec

Title: US-09-980-771A-5
Perfect score: 3370
Sequence: 1 ALDIYVAAEYAPWKTGGL.....SASKTSAAXPLVSAATRKSA 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3366	99.9	708	10	O64925	O64925 chlamydomon
2	1463.5	43.4	613	10	O93YB1	O93YB1 pisum sativ
3	1450.5	43.0	604	10	O9FR03	O9FR03 perilla fru
4	1424.5	42.3	608	10	O93VD9	O93VD9 ipomoea bat
5	1423.5	42.2	606	10	O9XIS6	O9XIS6 phaseolus v
6	1423.5	42.2	607	10	O92SQ5	O92SQ5 astragalus
7	1404	41.7	608	10	O8VYU1	O8VYU1 oryza sativ
8	1397.5	41.5	609	10	O94LY7	O94LY7 oryza sativ
9	1395.5	41.4	603	10	O8SA49	O8SA49 hordeum vul
10	1390	41.2	610	10	O9MAQ0	O9MAQ0 arabidopsis
11	1389.5	41.2	609	10	O8S9C4	O8S9C4 oryza sativ
12	1381	41.0	605	10	O9SXX3	O9SXX3 triticum ae
13	1380	40.9	605	10	O9FU06	O9FU06 triticum ae
14	1379	40.9	599	10	O9SQ58	O9SQ58 triticum ae
15	1376	40.8	606	10	O43012	O43012 oryza sativ
16	1375	40.8	604	10	O9S7N5	O9S7N5 triticum ae

17	1371	40.7	534	10	O8W2G8	O8W2G8 triticum ae
18	1369	40.6	604	10	O9SL56	O9SL56 triticum tu
19	1367.5	40.6	604	10	O9SL57	O9SL57 triticum tu
20	1367	40.6	605	10	O9SQ51	O9SQ51 aegilops sp
21	1366	40.5	605	10	O9SL58	O9SL58 triticum tu
22	1362.5	40.4	604	10	O9SXX4	O9SXX4 triticum ae
23	1360.5	40.4	604	10	O9SL59	O9SL59 triticum tu
24	1354.5	40.2	605	10	O9SQ52	O9SQ52 triticum mo
25	1353.5	40.2	574	10	O9SVU0	O9SVU0 triticum ae
26	1263.5	37.5	565	10	O9XEN9	O9XEN9 triticum ae
27	898	26.6	792	10	O9MAC8	O9MAC8 arabidopsis
28	895.5	26.6	313	10	O9LKD3	O9LKD3 vaquelinia
29	893.5	26.5	313	10	O9LKE0	O9LKE0 prunus virg
30	893.5	26.5	313	10	O9FYU8	O9FYU8 aruncus dio
31	891.5	26.5	647	10	O9LEB9	O9LEB9 triticum ae
32	891.5	26.5	647	10	O9SQH0	O9SQH0 aegilops ta
33	891.5	26.5	647	10	O9SQG9	O9SQG9 triticum ae
34	890.5	26.4	647	10	O9LEC0	O9LEC0 triticum ae
35	886.5	26.3	313	10	O9LKE8	O9LKE8 kageneckia
36	886	26.3	576	10	O64926	O64926 chlamydomon
37	885.5	26.3	313	10	O9LKD1	O9LKD1 exochorda r
38	884.5	26.2	643	10	O9M5A3	O9M5A3 hordeum vul
39	879.5	26.1	313	10	O9LKE5	O9LKE5 amelanchier
40	879.5	26.1	313	10	O9LKD6	O9LKD6 vaquelinia
41	878.5	26.1	313	10	O9LKE7	O9LKE7 kageneckia
42	878.5	26.1	313	10	O9LKE1	O9LKE1 prinsepia s
43	877.5	26.0	313	10	O9LKE6	O9LKE6 malus sarge
44	877.5	26.0	313	10	O9LKD8	O9LKD8 rosa multif
45	876.5	26.0	313	10	O9LKE5	O9LKE5 oemleria ce

ALIGNMENTS

RESULT 1
O64925 PRELIMINARY; PRT; 708 AA.
ID O64925
AC O64925;
DT 01-AUG-1998 (TREMREL.07, Created)
DT 01-DEC-2001 (TREMREL.19, Last sequence update)
DT 01-MAR-2002 (TREMREL.20, Last annotation update)
DE Granule-bound starch synthase I precursor (EC 2.4.1.21).
GN STA2.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137C;
RA D'Hulst C., Wattlebled F., Ral J.-P., Abel G.J., Kossmann J.,
RA Ball S.G.;
RT "Cloning of a cDNA encoding for the GBSI in the green alga
RT Chlamydomonas reinhardtii."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wattlebled F., Ball S.G., D'Hulst C.;
RA "Granule-bound starch synthase I: A major enzyme involved in the
RT biogenesis of B-crystallites in starch granules."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026420; AAC1969.3; -;
DR EMBL; AF433156; AAL28128.1; -;
DR InterPro; IPR001296; Glycos.transf.1.
DR InterPro; IPR002114; HPT_Serp_site.
DR Pfam; PF00534; Glycos.transf.1; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
KW Glycosyltransferase; Transferrase; TRANSIT.
FT CHAIN 1 57 POTENTIAL.
SQ SEQUENCE 708 AA; 74623 MW; 7D2A5A07D8606469 CRC64;

Query Match 99.9%; Score 3366; DB 10; Length 708;

Best Local Similarity 99.8%; Pred. No. 4.5e-190;
Matches 650; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALDVMVAEVPWSKGTGLGVDVGGPLPIELVYKGRHVMVTIAPRYDOYADAWDTSVVVDI 60
Db 58 ALDVMVAEVPWSKGTGLGVDVGGPLPIELVYKGRHVMVTIAPRYDOYADAWDTSVVVDI 117

QY 61 MGKRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKKRALCKAA 120
Db 118 MGKRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKKRALCKAA 177

QY 121 IEAARVLPFGEDCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLAHNTAFQGRMW 180
Db 178 IEAARVLPFGEDCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLAHNTAFQGRMW 237

QY 181 EFAKDTKLPQAFDKLAFSDGYAKVYTEATPMEDEKPLTGKTKYKINLWKGGLIAD 240
Db 238 EFAKDTKLPQAFDKLAFSDGYAKVYTEATPMEDEKPLTGKTKYKINLWKGGLIAD 297

QY 241 KLVTSVPNTATEIAAAGGVELDTVIRAKGIEGIVNGMDIEENPKTDKFLSAPYDQNS 300
Db 298 KLVTSVPNTATEIAAAGGVELDTVIRAKGIEGIVNGMDIEENPKTDKFLSAPYDQNS 357

QY 301 VYAGKAAAEALQAEGLGVPDTPAPLFAFVIGRLEBKQGVDIILAAALPKILATPKVOIAIL 360
Db 358 VYAGKAAAEALQAEGLGVPDTPAPLFAFVIGRLEBKQGVDIILAAALPKILATPKVOIAIL 417

QY 361 GTGKAAEYKLVNAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSRPEPCGLIOLHAM 420
Db 418 GTGKAAEYKLVNAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSRPEPCGLIOLHAM 477

QY 421 HYGTVPVASTGLGVDVTKGVTGFMGALNPKLDEADADALAAATVRRASEVFAGRYP 480
Db 478 HYGTVPVASTGLGVDVTKGVTGFMGALNPKLDEADADALAAATVRRASEVFAGRYP 537

QY 481 EMVANCISODLSWSKPAQWEGLEEVYKGGVATAKKEEIKVPVAEKIPGLPAVSYA 540
Db 538 EMVANCISODLSWSKPAQWEGLEEVYKGGVATAKKEEIKVPVAEKIPGLPAVSYA 597

QY 541 PNTLKPVSASVEGNGAAAPKVGTPAPAGAWRATTPSGPSPAAATPKVTYKPAKPATAK 600
Db 598 PNTLKPVSASVEGNGAAAPKVGTPAPAGAWRATTPSGPSPAAATPKVTYKPAKPATAK 657

QY 601 PKTAGLKLAGEASTTTSENGAASNGNGASASKTSAAKPLVSAATRKA 651
Db 658 PKTAGLKLAGEASTTTSENGAASNGNGASASKTSAAKPLVSAATRKA 708

RESULT 2
Q93YB1 PRELIMINARY; PRT; 613 AA.

ID Q93YB1
AC Q93YB1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Granule-bound starch synthase (EC 2.4.1.11).
GN GBSSI.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Edwards A., Vincken J.P., Visser R., Zeeman S., Smith A.M., Martin C.;
RT "Discrete forms of amylose are synthesised by isoforms of GBSSI in
pea.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ345045; CAC69955.1; -
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR001917; Ntrtransf_2.
DR Pfam; PF00534; Glycos_transf_1; 1.

DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
KW Glycosyltransferase; Transferase; Transf. No. 4.1e-78;
FT TRANSIT 1 85
FT CHAIN 86 613 GRANULE BOUND STARCH SYNTHASE.
SQ SEQUENCE 613 AA; 67626 MW; 5A653461128F97EB CRC64;

Query Match 43.4%; Score 1463.5; DB 10; Length 613;
Best Local Similarity 53.0%; Pred. No. 4.1e-78;
Matches 291; Conservative 74; Mismatches 137; Indels 47; Gaps 11;

QY 2 LDIVMVAEVPWSKGTGLGVDVGGPLPIELVYKGRHVMVTIAPRYDOYADAWDTSVVVDI- 60
Db 87 MNLFFVGTETAPWSKGTGLGVDVGGPLPIELVYKGRHVMVTIAPRYDOYADAWDTSVVVDI 146

QY 61 ---MGKRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKKRALFC 117
Db 147 VGRTEKRVFFHCFKRGVDVDFVDFHPIFEKVGKGTGKLYGAAGDDYQDNQLRSIFC 206

QY 118 KAAIEAARVLPF-----GP-GEDEVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLA 169
Db 207 QAAIEAARVNLKSNKYFSGPYGEDVILFVANDWHSALISCYMKSMYQSIGIFRNAKVFC 266

QY 170 IHNIAFGRMWEAFAKD---TKLPQAFDKLAFSDGYAKVYTEATPMEDEKPLTGKTY 226
Db 267 IHNIAFGRMWEAFAKD---TKLPQAFDKLAFSDGYAKVYTEATPMEDEKPLTGKTY 306

QY 227 KTNLWKGGLIADKLVTSVPNTATEIAAAGGVELDTVIRAKGIEGIVNGMDIEENWP 286
Db 307 RKNWKGGLIADKLVTSVPNTATEIAAAGGVELDTVIRAKGIEGIVNGMDIEENWP 366

QY 287 KTKFISAPYDQNSVYAGKAAAEALQAEGLGVPDTPAPLFAFVIGRLEBKQGVDIILAAAL 346
Db 367 STDKYSISIKYDASTVLEKALKEELQAEVCLPVDKNVPLIAFVIGRLEBKQGVDIILAAAL 426

QY 347 PKILATPKVOIAILGTGKAAEYKLVNAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPS 406
Db 427 PQFI-KENVOIIVAGTGKKEEKLQAEGLGVPDTPAPLFAFVIGRLEBKQGVDIILAAAL 485

QY 407 SRPEPCGLIOLHAMHYGTVPVASTGLGVDVTKGVTGFMGALNPKLDEADADALAAAT 464
Db 486 SRPEPCGLIOLHAMHYGTVPVASTGLGVDVTKGVTGFMGALNPKLDEADADALAAAT 545

QY 465 ATVRRASEVFAGRYPVEMVANCISODLSWSKPAQWEGLEEVYKGGVATAKKEEIKVP 516
Db 546 KVTYKALGVYGTSAFAEMIKNCMAQELSWKGPAPKKEEVLNGLVDPSEPDIDGQ-ETAP 604

QY 517 AKKEIKVP 525
Db 605 QAKENATP 613

RESULT 3
Q9FR03 PRELIMINARY; PRT; 604 AA.

ID Q9FR03
AC Q9FR03
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Granule-bound starch synthase.
GN GBSSI.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. OKDONG; TISSUE=DEVELOPING SEEDS;
RA Hwang S.-K., Hwang Y.-S.;
RT "Isolation and characterization of a cDNA encoding granule-bound
starch synthase from Perilla frutescens.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210699; AAG43519.1; -

```

DR InterPro: IPR001296; Glycos_transf_1.
DR Pfam: PF00534; Glycos_transf_1; 1.
SQ SEQUENCE 604 AA; 66214 MW; 435CE9601C85A5EF CRC64;

Query Match      43.0%; Score 1450.5; DB 10; Length 604;
Best Local Similarity 54.3%; Pred. No. 2.3e-77;
Matches 297; Conservative 62; Mismatches 145; Indels 43; Gaps 10;

QY 2 LDIVMVAEAVPNSKSGGLGDDVTGGLPIELVVKGRHVRMTIAPRYDQYADAWDTSVVVDI- 60
Db 78 MTLIFVSAEGPGSGGLGDDVYVGLPPLAANRHRVMTSPRYDQYKDAWDTSVVVEIQ 137
QY 61 MGEKVR---YFHSIKKGVHRVWDHPWFLAKVWGKSGKLYGPRSGADYLDNKRKRALFC 117
Db 138 VGDKVTVEGFFHCYKKGVDVFDHPLFLKGVGKTSKVGYSAGVDYEDNQLRFLSLS 197
QY 118 KAIEAARVLFP-----GP-GEDCVFVANDWHSALVPLVLLKDEYOPKGOFTKAKSVLA 169
Db 198 LALEAPRVNLNTSNKYFSGPYGEDVVFVANDWHTAIVLPCYLTIQPKGIYNNAKVLC 257
QY 170 IHNIAFOGRWEEAFKDTKLPOAFDKLAFSDGYAKVYVTEATPMEDEKPLTGKTYKKI 229
Db 258 IHNIAFGRAFSDFLKLNLPDQLKSSDFMDGYE-----PVKG---RKI 300
QY 230 NMLKGGTIAADKLVTSVPNATETADAAGGVLDVTIRAKGTGIVNGMDIEWNPKTID 289
Db 301 NNMKAGIESDRVLTVPYANELVSGPKGVLDNMLRKCTVTGIVNGMDTQEWNPATD 360
QY 290 KFLSAPYDQNSVYAGAAAEALQAEGLPDPVTPAFIFGRLEEQKGVDTIILALPKI 349
Db 361 KYIDNHYDITVMDGRPLKKEALQAEVGLPVDNRNPLVGLFGRLEEQKGSIIILVAHKF 420
QY 350 LATPKVQIALLGTGKAAYEKLVNAIGTKYGRAGKGVVKSAPLAHMLTAGADPMLVPSRF 409
Db 421 IEM-DVQVILGTGKKEFEQIEQLEVMYPDKARGVAKFNVPLAHMTITAGADPMLVPSRF 479
QY 410 EPCGLIQLHAMHYGTVPVASTGGIVDTVKEGTVGFHMGALNP--DKLEADADALAATV 467
Db 480 EPCGLIQLHAMRYGTIPICASTGGIVDTVKEGTVGFHMGAFNVNVEDADPADVLKIVTIV 539
QY 468 RRASEVFAGRPYEMVANCISDLSWSKPAQKWEGLLEEVYVKGK-----VATAK 518
Db 540 GRALEYGTPAPFEMINNCMSLDLSWKGPAKNWETVL--LSLGVAGSEPGVEGDEAPLA 597
QY 519 KEEIKVP 525
Db 598 KENVATP 604

RESULT 4
Q93VD9 PRELIMINARY; PRT; 608 AA.
AC Q93VD9;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Granule-bound starch synthase I (EC 2.4.1.21).
GN GBSI.
OS Ipomoea batatas (Sweet potato) (Batata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=4120;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. KOREI 14;
RA Kimura T., Saito A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. KOREI 14;
RA Kimura T., Ideta O., Saito A.;
RT *Identification of the gene encoding granule-bound starch synthase I

in sweet potato (Ipomoea batatas (L.) Lam.).";
Plant Biotechnol. 17:247-252(2000).
DR EMBL; AB071976; BAB68525.1; -
DR EMBL; AB071604; BAB68126.1; -
DR InterPro: IPR001296; Glycos_transf_1.
DR Pfam: PF00534; Glycos_transf_1; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 608 AA; 66689 MW; C93CDA49A1F50C03 CRC64;

Query Match      42.3%; Score 1424.5; DB 10; Length 608;
Best Local Similarity 55.6%; Pred. No. 7.9e-76;
Matches 293; Conservative 61; Mismatches 150; Indels 43; Gaps 10;

QY 2 LDIVMVAEAVPNSKSGGLGDDVTGGLPIELVVKGRHVRMTIAPRYDQYADAWDTSVVVDI- 60
Db 82 MNLVFCGCEVGPCKTGGGLGDLPLPALAARHVRVTCPRYDQYKDAWDTCVVVEIQ 141
QY 61 MG---EKVYFHSIKKGVHRVWDHPWFLAKVWGKSGKLYGPRSGADYLDNKRKRALFC 117
Db 142 VGDRIEVPREFHSHYKRGVDRVFDHPLFLKGVGKTSKLYGPRSGADYLDNKRKRALFC 201
QY 118 KAIEAARVLFP-----GP-GEDCVFVANDWHSALVPLVLLKDEYOPKGOFTKAKSVLA 169
Db 202 QAALAPRVNLNTSNKYFSGPYGEDVVFVANDWHTALLPCYLTMYOSRGIYNNAKVAF 261
QY 170 IHNIAFOGRWEEAFKDTKLPOAFDKLAFSDGYAKVYVTEATPMEDEKPLTGKTYKKI 229
Db 262 IHNIAFGRAFSDFLKLNLPDQKSSDFMDGYE-----PVKG---RKI 304
QY 230 NMLKGGTIAADKLVTSVPNATETADAAGGVLDVTIRAKGTGIVNGMDIEWNPKTID 289
Db 305 NNMKAGITREADRVTVSPNATETAKELVSCVSGVELDNHIDCGITGICNGMDTQEWNPATD 364
QY 290 KFLSAPYDQNSVYAGAAAEALQAEGLPDPVTPAFIFGRLEEQKGVDTIILALPKI 349
Db 365 KYLAVKYDITVMDGRPLKKEALQAEVGLPVDNRNPLVGLFGRLEEQKGSIIILVAISKF 424
QY 350 LATPKVQIALLGTGKAAYEKLVNAIGTKYGRAGKGVVKSAPLAHMLTAGADPMLVPSRF 409
Db 425 ISM-DVQVILGTGKKEFEQIEQLEVMYPDKARGVAKFNVPLAHMTITAGADPMLVPSRF 483
QY 410 EPCGLIQLHAMHYGTVPVASTGGIVDTVKEGTVGFHMGALNP--KLEADADALAATV 467
Db 484 EPCGLIQLHAMRYGTIPICASTGGIVDTVKEGTVGFHMGAFNVNVEDADPADVLKIVTIV 543
QY 468 RRASEVFAGRPYEMVANCISDLSWSKPAQKWEGLLEEVYVKGK-----VATAK 518
Db 544 GRALAMYGLAFTTEMKNCMSQELSWSKPAKNWETVL--LSLGVAGSEPGVEGDEAPLA 601
QY 519 KEEIKVP 525
Db 602 KENVATP 608

RESULT 5
Q9XIS6 PRELIMINARY; PRT; 606 AA.
AC Q9XIS6;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Granule-bound starch synthase I precursor (EC 2.4.1.21).
GN GBSI.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE FROM N.A.
RA ISONO N., Nozaki K., Ito H., Matsui H., Honma M.;
RT "Phaseolus vulgaris L. mRNA for Granule-Bound Starch Synthase I
(GBSI).";

```


Query Match 41.7%; Score 1404; DB 10; Length 608;
 Best Local Similarity 51.5%; Pred. No. 1.3e-74;
 Matches 283; Conservative 72; Mismatches 147; Indels 48; Gaps 10;

QY 2 LDIWMAAEVAPWSKTGGGLDVTGGGLPIELVKKGRHVRMTIAPRYDQYADAWDTSVVVDI- 60
 DB 81 MTIIFATECHPWCKTGGGLDVLGGLPPLAAMGHRVMTIPRYDQYADAWDTNVLVEVN 140
 QY 61 ---MGEKRVYFHSIKGVRHVRWIDHPWFLAKVWCKTSGSKLYGRSGADYLDNKKRALFC 117
 DB 141 IGRDTEVRFCHYKRGVDRFVDPHFMFLKGVKGTGPKLYGPTGGDYRDNLRFCLLC 200
 QY 118 KAAIEARVLPF-----GP-GECDQVFNWHSALVLPVLLKDEYQPKQFTKAKSVLA 169
 DB 201 LALEAPRVLLNNSEYFSGPYGVNVFVANDWHTGVLPCYLKSIYQAKGMVNAKVAF 260
 QY 170 IHNIAFOGRMWEAFKDTKLPOAFAFKLAFSDGYAKVYTEATPMEDEKPLTGKTYKKI 229
 DB 261 IHNIAFOGRMWEAFKDTKLPOAFAFKLAFSDGYAKVYTEATPMEDEKPLTGKTYKKI 229
 QY 230 NWLKGGLIADKLVTSPNYATEIADAAGGVELDTVIRAKGIE-GIVNGMDIEEWNPKT 288
 DB 304 NWMKAGITECDLVMTSPVHYKELASGPDGKVELDGLIRTKPLETGIVNGMDVYENPAT 363
 QY 289 DKFLSAPYDQNSVYAGAAKAEALQELGLPDPDTAPLFAFIRGLEBQKGVDIILALPK 348
 DB 364 DQIISVKYDATTTEARALNKMLOAEVGLPVDSSIPLIIVFVGRLEBQKGVDIILALPK 423
 QY 349 ILATPKVOIAILGTGAAVEKLYNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVPSR 408
 DB 424 FV-EGNVQIIVLTGKMKKEELILEVKNPTARGLAKFNVLPAHMFAGADFIIVPSR 482
 QY 409 FEPCLGLIQLHAMHYGVVAVSTGGGLVDVTKEGVTGFHMGALNP--DKLEADADALAA 466
 DB 483 FEPCLGLIQLQMGRYGVVPCISSTGGGLVDVTKEGVTGFHMGALNP--DKLEADADALAA 542
 QY 467 VRASEVFAAGRYPEMVANCISODLSWSKPAQKWEGLLEEVYKGG-----GVA 515
 DB 543 VKRALQYNTAPQEQMVQNCMAODLSWKGPAAKKW----BEVLGLGVEGSGQPIEGEEVA 598
 QY 516 TAKKEIKVP 525
 DB 599 PLAKENVATP 608

RESULT 8
 Q94LY7
 ID Q94LY7 PRELIMINARY; PRT; 609 AA.
 AC Q94LY7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE Granule-bound starch synthase (EC 2.4.1.21).
 GN WAXY.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. REXMONT.
 RA Larkin P.D., McClung A.M., Ayres N.M., Park W.D.;
 RT "The Wx locus (Granule Bound Starch Synthase) is strongly associated
 with pasting curve characteristics in rice (Oryza sativa L.).";
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF141954; AAF72561.1;
 DR InterPro; IPR001296; Glycos.transf.1.
 DR Pfam; PF00534; Glycos.transf.1.
 DR PROSITE; PS00606; B_KETOACYL-SYNTHASE; UNKNOWN.1.
 SQ SEQUENCE 609 AA; 66466 MW; 6D2615EB203CB0D8 CRC64;

Query Match 41.4%; Score 1395.5; DB 10; Length 603;
 Best Local Similarity 53.3%; Pred. No. 4e-74;
 Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;

QY 2 LDIWMAAEVAPWSKTGGGLDVTGGGLPIELVKKGRHVRMTIAPRYDQYADAWDTSVVVDI- 60
 DB 83 MNVFEVGAEMAPWSKTGGGLDVLGGLPPLAAMGHRVMTIPRYDQYADAWDTSVVVAEK 142
 QY 61 ---MGEKRVYFHSIKGVRHVRWIDHPWFLAKVWCKTSGSKLYGRSGADYLDNKKRALFC 117
 DB 143 VADRYERVRFFCHYKRGVDRFVDPHFMFLKGVKGTGPKLYGPTGGDYRDNLRFCLLC 200
 QY 118 KAAIEARVLPF-----PFGP-GECDQVFNWHSALVLPVLLKDEYQPKQFTKAKSVLA 169
 DB 203 QAALEAPRVLLNNSEYFSGPYGVNVFVANDWHTGVLPCYLKSIYQAKGMVNAKVAF 262
 QY 170 IHNIAFOGRMWEAFKDTKLPOAFAFKLAFSDGYAKVYTEATPMEDEKPLTGKTYKKI 229
 DB 263 IHNISYOGRAFEDYDELNLSEFRSSFDIDGY-----DTPVEG-----RKI 305
 QY 230 NWLKGGLIADKLVTSPNYATEIADAAGGVELDTVIRAKGIEGIVNGMDIEEWNPKTD 289
 DB 306 NWMKAGILEADLVMTSPVHYKELASGPDGKVELDGLIRTKPLETGIVNGMDVSEWDPK 365
 QY 290 KFLSAPYDQNSVYAGAAKAEALQELGLPDPDTAPLFAFIRGLEBQKGVDIILALPKI 349
 DB 366 KYITAKYDATTAEAKALKEALQAEAGLIPVGRKIPLIATIGRLEBQKGVDIILALPKI 425
 QY 350 LATPKVOIAILGTGAAVEKLYNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVPSRF 409
 DB 426 M-OEDVQIIVLTGKMKKEELILEVKNPTARGLAKFNVLPAHMLTAGADFMVPSRF 484
 QY 410 EPGCLLIQLHAMHYGVVAVSTGGGLVDVTKEGVTGFHMGALNP--KLDEADADALAA 467
 DB 485 EPGCLLIQLQMGRYGVVPCISSTGGGLVDVTKEGVTGFHMGALNP--KLDEADADALAA 544
 QY 468 VRASEVFAAGRYPEMVANCISODLSWSKPAQKWEGLLEEVYKGG-----VATAK 518
 DB 545 KRAIKVVGTPAYEEMVYRNCMDLSWKGPAAKKWNL--LGLGVAGSAPGIEGDEIAPLA 602
 QY 519 KPEIKVP 525
 DB 603 KENVAAP 609

RESULT 9
 Q8SA49
 ID Q8SA49 PRELIMINARY; PRT; 603 AA.
 AC Q8SA49;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Granule-bound starch synthase.
 GN 259116.5.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. MEREX;
 RA Ma J., SanMiguel P.J., Dubcovsky J., Shiloff B.A., Rostoks N.,
 RA Jiang Z., Buss C.S., Kleinbols A., Devos K.M., Ramakrishna W.,
 RA Bennett J.L.;
 RT "Comparative sequence analysis of Wx1 homologous regions in barley,
 maize, pearl millet, rice, sorghum and diploid wheat.";
 RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF474373; AAL77109.1;
 SQ SEQUENCE 603 AA; 66280 MW; 467A3DE6A82125CB CRC64;

Matches 277; Conservative 71; Mismatches 141; Indels 31; Gaps 7;

QY 2 LDIVMVAEAVPWSKTGGLGVDVGTGLPIELVKRGHRVMTIAPRYDQYADAWDTISVVVDIM 61
 Db 76 MNLVFGAEMAPWSKTGGLGVDVGTGLPIELVKRGHRVMTIAPRYDQYADAWDTISVSEIK 135
 QY 62 ---GEKRYFHSIKKGVHRVWIDHPWFLAKYWGKSGKLYGPRSGADYLDNHRKFAFPC 117
 Db 136 VADEYERVFHCYKRGVDRVIDHPWFLAKYWGKSGKLYGPRSGADYLDNHRKFAFPC 195
 QY 118 KAAIEAARVLPF---GP-GEDEVFVANDHWSALVPLVLLKDEYQKQGTAKAKSVLA 169
 Db 196 QAAIEAARVLPF---GP-GEDEVFVANDHWSALVPLVLLKDEYQKQGTAKAKSVLA 255
 QY 170 IHNIAFOGRMFEAFKDTKLP---QAAFDKLAFCGYAKVYTEATPMEDEKPLTGKTYKI 229
 Db 256 IHNIAFOGRMFEAFKDTKLP---QAAFDKLAFCGYAKVYTEATPMEDEKPLTGKTYKI 298
 QY 230 NMLKGGIITAADKLVTVSPNYATEIAADAAGGVDELDTVIRAKGIEGIVNGMDIEBNP 289
 Db 299 NMLKGGIITAADKLVTVSPNYATEIAADAAGGVDELDTVIRAKGIEGIVNGMDIEBNP 358
 QY 290 KFLSAPYDONSIVAGKAAKAEALQAEGLPVDPTAPLFAFIFGRLEBQKGVDIILAALPKI 349
 Db 359 KFLSAPYDONSIVAGKAAKAEALQAEGLPVDPTAPLFAFIFGRLEBQKGVDIILAALPKI 418
 QY 350 LATPKVQIATLGTGKAAEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADEMCLVPSRF 409
 Db 419 LKEDVQIILLGTGKAAEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADEMCLVPSRF 478
 QY 410 EPCGLIQLHAMHYGTPVAVASTGGLVDTVKEGVTGPHMGALNP--DKLDEADADALA 467
 Db 479 EPCGLIQLHAMHYGTPVAVASTGGLVDTVKEGVTGPHMGALNP--DKLDEADADALA 538
 QY 468 RRASEVFAGCRPEMVAANCISQDLSWSKPAQKWEGLLEEV 507
 Db 539 KRAVYGVGTPAYOEMVKNCMQDLSWSKPAQKWEGLLEEV 578

RESULT 10
 Q9MAQ0
 ID Q9MAQ0 PRELIMINARY; PRT; 610 AA.
 AC Q9MAQ0
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Granule-bound starch synthase.
 GN P9111.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLOMBIA;
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altati H., Nguyen M., Lam B., Southwick A., Bei, Buchler E., Chin C.,
 RA Chion J., Choi E., Dunn P., Gonzalez A., Howng B., Kim C., Koo T.,
 RA Lee J.M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Piam P., Sakano H., Schwartz J., Shinn P., Thaveri A., Toriumi M.,
 RA Vaysberg M., Walker M., Yu G., Ecker M., Theologis A., Davis R.W.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006424; AAF31273.1;
 DR InterPro; IPR001296; Glycos.transf.1.
 DR Pfam; PF00534; Glycos.transf.1.1.
 DR SEQUENCE 610 AA; 65879 MW; CF17F25BE12220DF CRC64;

Query Match 41.2%; Score 1390; DB 10; Length 610;
 Best Local Similarity 52.7%; Pred. No. 8.6e-74;
 Matches 287; Conservative 72; Mismatches 146; Indels 40; Gaps 12;

QY 2 LDIVMVAEAVPWSKTGGLGVDVGTGLPIELVKRGHRVMTIAPRYDQYADAWDTISVVVDI- 60
 Db 83 MNLVFGAEMAPWSKTGGLGVDVGTGLPIELVKRGHRVMTIAPRYDQYADAWDTISVSEIK 142
 QY 61 ---MGEKRYFHSIKKGVHRVWIDHPWFLAKYWGKSGKLYGPRSGADYLDNHRKFAFPC 117

RESULT 11
 Q8S9C4
 ID Q8S9C4 PRELIMINARY; PRT; 609 AA.
 AC Q8S9C4
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Starch granule-bound starch synthase.
 GN WX-1.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. MILKY QUEEN;
 RA Sato H., Suzuki Y., Sakai M., Imbe T.;
 RT "Molecular Characterization of wx-1, a Novel Mutant Gene for Low-
 amylose Content in Endosperm of Rice (Oryza sativa L.).";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB066093; BAB88209.1;
 DR SEQUENCE 609 AA; 66431 MW; B57CC13E0440D227 CRC64;

Query Match 41.2%; Score 1389.5; DB 10; Length 609;
 Best Local Similarity 51.2%; Pred. No. 9.2e-74;
 Matches 280; Conservative 76; Mismatches 148; Indels 43; Gaps 9;

QY 2 LDIVMVAEAVPWSKTGGLGVDVGTGLPIELVKRGHRVMTIAPRYDQYADAWDTISVVVDI- 60
 Db 83 MNLVFGAEMAPWSKTGGLGVDVGTGLPIELVKRGHRVMTIAPRYDQYADAWDTISVSEIK 142
 QY 61 ---MGEKRYFHSIKKGVHRVWIDHPWFLAKYWGKSGKLYGPRSGADYLDNHRKFAFPC 117


```

Db 143 VADRYRVRFFHCYKHGVDVRFIDHPSELEKVGKTEKTIYDPTGVDHKNQMFSLIC 202
QY 118 KAAEAAARVL-----PFGP-----GECVFNVDHWSALVPVLLKDEYQPKGQFTAKSVLA 169
Db 203 QAALEAPRILNINNPFYKTYGDEVFVPCNDWHTGPLASVYLNKNYQPNGIYRNKAVAF 262
QY 170 IHNIAFGRMWEEAFKDKLPQAAFDKLAFLSDGAKVYVTEATPMEDEKPLTKYTKKI 229
Db 263 IHNISYQGRFAFEDYPELUNSERPSRSDFDIDGY-----DTPVEG-----RKI 305
QY 230 NWLKGIIAADKLVTSVSPNYATEIAADAAGVVELDTVIRAKGIEGIVNGMDIEENPKTD 289
Db 306 NWMKAGILEADRLVTSVSPYAEELISGTARCELDNIMRLTGITGIVNGMDVSEWDPK 365
QY 290 KFLSAPYDONSIVYAKAAKALQAEGLPVDPTAPLFAFTGRLEEQKGVDIILAAALPKI 349
Db 366 KYITAKYDATTAEBAKALNKEALQAEGLPVDRIPLIATFTGRLEEQKGVDPVMAAIIPEL 425
QY 350 LATPKVQITAILGTGKAAVEKLVNAIGTKYGRKGVVVFESAPLAHMLTAGADFMVPSRF 409
Db 426 M-QEDVOIVLLGTGKKEFERLLKSVYEEKPSKVRVAVRNAPLAHLMAGADVLAITSRF 484
QY 410 EPCGLIOLHAMHYGTVPVASTGGGLVDTVKEGVTGFHMGALNPD--KLDEADADALAATV 467
Db 485 EPCGLIOLQGMRYGTGTPCACASTGGGLVDTVIEGKTGFHMGRLSVDCVKEPSDVKKVAATL 544
QY 468 RRASEVPAGGRYPPEMVANCIQSOLSWSPKPAQKWEGLLEEVYVYKGG-----VATAK 518
Db 545 KRAIKVGTGTAYEEMVENCNODLSWKGPAKNWENVL--LGLGVAGSAPGIEGDEIAPLA 602
QY 519 KEIKVP 525
Db 603 KENVAAP 609

```

RESULT 12

```

Q9SXK3 ID Q9SXK3 PRELIMINARY; PRT; 605 AA.
AC Q9SXK3;
DT 01-MAY-2000 (TremBrel. 13, Created)
DT 01-JUN-2002 (TremBrel. 13, Last sequence update)
DE 01-JUN-2002 (TremBrel. 21, Last annotation update)
DE Starch synthase (GBSSI) (EC 2.4.1.21).
GN WAXY.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99321800; PubMed-10393240;
RA Murai J., Taira T., Ohta D.;
RT "Isolation and characterization of the three waxy genes encoding the
RL granule-bound starch synthase in hexaploid wheat.";
RL Gene 234:71-79(1999).
DR EMBL; AB019623; BAA77351.1; -
DR InterPro; IPR001296; Glycos.transf_1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycos.transf_1; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 605 AA; 66345 MW; 60A816276F78722B CRC64;

```

```

Query Match 41.0%; Score 1381; DB 10; Length 605;
Best Local Similarity 51.5%; Pred. No. 2.9e-73;
Matches 281; Conservative 72; Mismatches 153; Indels 40; Gaps 9;

```

```

QY 2 LDIVVAAEVAEPWPKSGTGGGLDVTGGLPIELVKRHRVMTIAPRYDQYADAWDTSVVVDIM 61
Db 78 MNLVFGAEMAPWSKTGGGLDVLGGIPLPAMAANGHRVMTISPRYDQYKDAWDTSVVSEIK 137

```

```

QY 62 ----GEKRYFHSIKKGVRVWIDHPFLAKVWGTGSKLYGPRSGADYLDNHRKFAFLFC 117
Db 138 VADEYRVRYFHCYKRGVDVRFIDHPSELEKVGKTEKTIYDPTGVDHKNQMFSLIC 197
QY 118 KAAEAAARVL-----PFGP-----GECVFNVDHWSALVPVLLKDEYQPKGQFTAKSVLA 169
Db 198 QAALEAPRILNINNPFYKTYGDEVFVPCNDWHTGPLASVYLNKNYQPNGIYRNKAVAF 257
QY 170 IHNIAFGRMWEEAFKDKLPQAAFDKLAFLSDGAKVYVTEATPMEDEKPLTKYTKKI 229
Db 258 IHNISYQGRFAFEDYPELUNSERPSRSDFDIDGY-----DTPVEG-----RKI 300
QY 230 NWLKGIIAADKLVTSVSPNYATEIAADAAGVVELDTVIRAKGIEGIVNGMDIEENPKTD 289
Db 301 NWMKAGILEADRLVTSVSPYAEELISGTARCELDNIMRLTGITGIVNGMDVSEWDPK 360
QY 290 KFLSAPYDONSIVYAKAAKALQAEGLPVDPTAPLFAFTGRLEEQKGVDIILAAALPKI 349
Db 361 KYITAKYDATTAEBAKALNKEALQAEGLPVDRIPLIATFTGRLEEQKGVDPVMAAIIPEI 420
QY 350 LATPKVQITAILGTGKAAVEKLVNAIGTKYGRKGVVVFESAPLAHMLTAGADFMVPSRF 409
Db 421 LKEEDVOIVLLGTGKKEFERLLKSVYEEKPSKVRVAVRNAPLAHLMAGADVLAITSRF 480
QY 410 EPCGLIOLHAMHYGTVPVASTGGGLVDTVKEGVTGFHMGALNPD--KLDEADADALAATV 467
Db 481 EPCGLIOLQGMRYGTGTPCACASTGGGLVDTVIEGKTGFHMGRLSVDCVKEPSDVKKVVTTL 540
QY 468 RRASEVPAGGRYPPEMVANCIQSOLSWSPKPAQKWEGLLEEV-----VYKGGVATAKK 519
Db 541 KRAIKVGTGTAYEEMVENCNODLSWKGPAKNWENVL--LGLGVAGSAPGIEGDEIAPLA 599
QY 520 BEIKVP 525
Db 600 ENVAAP 605

```

RESULT 13

```

Q9FU06 ID Q9FU06 PRELIMINARY; PRT; 605 AA.
AC Q9FU06;
DT 01-MAR-2001 (TremBrel. 16, Created)
DT 01-MAR-2001 (TremBrel. 16, Last sequence update)
DE 01-JUN-2002 (TremBrel. 21, Last annotation update)
DE Granule bound starch synthase I (EC 2.4.1.21).
GN GBSSI.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-CV. CHEYENNE; TISSUE-ENDOSPERM;
RA McCue K.F., Hurkman W.J., Tanaka C.K., Anderson O.D.;
RT "Starch Branching Enzymes Sbe1 and Sbe2 from Wheat (Triticum aestivum
RL cv. Cheyenne): Molecular Characterization, Developmental Expression,
RL and Homolog Assignment by Differential PCR.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286320; AAG27624.1; -
DR InterPro; IPR001296; Glycos.transf_1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycos.transf_1; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 605 AA; 66326 MW; 21120D9D6F68B891 CRC64;

```

```

Query Match 40.9%; Score 1380; DB 10; Length 605;
Best Local Similarity 51.5%; Pred. No. 3.3e-73;
Matches 281; Conservative 72; Mismatches 153; Indels 40; Gaps 9;

```

```

QY 2 LDIVVAAEVAEPWPKSGTGGGLDVTGGLPIELVKRHRVMTIAPRYDQYADAWDTSVVVDIM 61
Db 78 MNLVFGAEMAPWSKTGGGLDVLGGIPLPAMAANGHRVMTISPRYDQYKDAWDTSVVSEIK 137

```

Db 78 NNLVEVGAEMAPWSKTGGGLDVLGGLPPAMAANGHRVMSIPRYDQYKDAWDTSVVSEIK 137
 QY 62 ----GEKVRYFHSIKGVRHWIDHFWFLAKYWGKSGSKLYGPRSGADYLDNHRKFAIPC 117
 Db 138 VADEYERVRFFHCYKRGVDVDFVDPFCFLEKVRGKTKKIKYIGPDAGTIDEDNOLRSLIC 197
 QY 118 KAAIEAARVL-----PF--GP--GEDCVFVANDHWSALVPLVLLKDEYQPRGQFTKAKSVLA 169
 Db 198 QAALEAPRILDLNNPYSFGYGVDFVFCNDWHITACLLACYLKSNSQSSGIYRTAKVAF 257
 QY 170 IHNIAFGQRMWEAFKDTKLQAAFDKLAFCSDGYAKVYTEATPMEDEKPPLTGKTKYKI 229
 Db 258 IHNISYQGRFSFDDFAQLNLPORFKSSDFIDYDK-----PVVG---RKI 300
 QY 230 NNLKGGIIAADKLVTVSPNYATAADAGGVELDTVIRAKGIEGIVNGMDIEWNPKT 289
 Db 301 NNLKAGILQADKLVTVSPYIAELISGEARGCELDNIMRLTGTGIVNGMDVSEWPAKD 360
 QY 290 KFLSAPYDONSYYAGKAAKALQALGELPVDPTAPLFAFIFGRLEQKGVDDIILALPKI 349
 Db 361 KFLAANYDVTTALLEGKALNKEALQAEVGLPVDKRVPLVAFVIGRLEQKGVDDVMAAIP 420
 QY 350 LATPKVQIALLGTGKAAAEKLYNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVPSRF 409
 Db 421 LKEDYQIYLLGTGKFFELLSVEEKFPSKVRVVRFNAPLAHQMGADVLAVTSRF 480
 QY 410 EPCGLIOLHAMHYGTVPVVASTGGGLVDTVYKGVTFGHMGALNPD--KLDEADADALAATV 467
 Db 481 EPCGLIOLQGMRYGTPCACASTGGGLVDTINTEKTFGHMGLSHLSDCNVVEPADVKVVTIL 540
 QY 468 RRASEVFAGGRYPPEMVANCTISQDLSWSKPAQKWEGLEEV-----VYKGGGVATAKK 519
 Db 541 KRAVKVGTGPAYHEMVKMCMQDLSWSKPAKKNWEDVLELGVGSEPGVIGE--EIAPLAM 599
 QY 520 EEIKVP 525
 Db 600 ENVAAP 605

RESULT 14
 Q9SQ58 PRELIMINARY; PRT; 599 AA.
 ID Q9SQ58
 AC Q9SQ58;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Granule-bound starch synthase GBSSI.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakamura T., Vrinten P.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF109395; AAF14233.1;
 DR InterPro; IPR001296; Glycos_transf_1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 KW Glycosyltransferase; Transferrase.
 SQ SEQUENCE 599 AA; 66045 MW; D486EFC90557F131 CRC64;

Query Match 40.9%; Score 1379; DB 10; Length 599;
 Best Local Similarity 50.4%; Pred. No. 3.7e-73;
 Matches 277; Conservative 78; Mismatches 147; Indels 48; Gaps 10;

QY 2 LDIWVAAEAPWSKTGGGLDVTGGLPIELVKGRHVMTIAPRYDOYADAWDTSVVVDI 61
 Db 72 MPILFVTEVHPWCCTGGGLGVVGLDLPALAAHGRVMTIAPRYDQYKDTWIDNVLVEVI 131
 QY 62 ----GEKVRYFHSIKGVRHWIDHFWFLAKYWGKSGSKLYGPRSGADYLDNHRKFAIPC 117
 Db 132 VGDTEYERVRFFHCYKRGVDVDFVDPFCFLEKVRGKTKKIKYIGPDAGTIDEDNOLRSLIC 191

QY 118 KAAIEAARVLPF-----GP--GEDCVFVANDHWSALVPLVLLKDEYQPRGQFTKAKSVLA 169
 Db 192 LAALEAPRVLNNSSEYFSGPYGENVFFVANDWHITAVLPCYLKSMYKONGIYYNAKVAFC 251
 QY 170 IHNIAFGQRMWEAFKDTKLQAAFDKLAFCSDGYAKVYTEATPMEDEKPPLTGKTKYKI 229
 Db 252 IHNIAFGQRPVRVDFELNLPESFMPSEDFVDCGHV-----PVVG---RKI 294
 QY 230 NNLKGGIIAADKLVTVSPNYATAADAGGVELDTVIRAKGIE--GIVNGMDIEWNPKT 288
 Db 295 NNLKAGITECDVLTVSPHYVKELTSPEKGVELDGLVRAKPLETGTGIVNGMDVVDNPNAT 354
 QY 289 KFLSAPYDONSYYAGKAAKALQALGELPVDPTAPLFAFIFGRLEQKGVDDIILALPK 348
 Db 355 DKYISVKYNATTVAERALNKEILOAEVGLPVDSSIPVIVFGRLEEQKGSILIAAIP 414
 QY 349 ILATPKVQIALLGTGKAAAEKLYNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVPSR 408
 Db 415 FL--EENVQIILVIGLGGKKKEEELMLEAKYPQVARGIAKENVPLAHMVFAGANFIIVPSR 473
 QY 409 FEPGLIOLHAMHYGTVPVVASTGGGLVDTVYKGVTFGHMGALNP--DKLDEADADALAAT 466
 Db 474 FEPGLIOLQGMRYGTVIPCSSTGGGLVDTVSEGTGFMGSGFNVEFETVDPADVAVASN 533
 QY 467 RRASEVFAGGRYPPEMVANCTISQDLSWSKPAQKWEGLEEVYKVG-----GVA 515
 Db 534 VTRALKQYKTPSFHAMVQNCMAQDLSWSKPAKKW---EBALLGLGVGSGQPIEGEIEA 589
 QY 516 TAKKEIKVP 525
 Db 590 PLAKONVATP 599

RESULT 15
 ID Q43012 PRELIMINARY; PRT; 606 AA.
 AC Q43012;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Starch granule-bound starch synthase (EC 2.4.1.11).
 GN WAXY.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SSP. L.F. SPONTANEA;
 RA Wang Z.Y., Zheng F.Q., Gao J.P., Wang X.Q., Wu M., Zhang J.L.,
 RA Hong M.M.;
 RT "Identification of two transposon-like elements in rice Wx gene."
 RL Sci. China B 37:437-447(1994).
 DR EMBL; X64108; CAA45472.1;
 DR InterPro; IPR001296; Glycos_transf_1.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 KW Glycosyltransferase; Transferrase.
 SQ SEQUENCE 606 AA; 66323 MW; E11157468A5553CE CRC64;

Query Match 40.8%; Score 1376; DB 10; Length 606;
 Best Local Similarity 50.7%; Pred. No. 5.7e-73;
 Matches 277; Conservative 77; Mismatches 148; Indels 44; Gaps 10;

QY 2 LDIWVAAEAPWSKTGGGLDVTGGLPIELVKGRHVMTIAPRYDOYADAWDTSVVVDI 60
 Db 83 MNVYVGAEMAPWSKTGGGLDVLGGLPPALAAHGRVMTIAPRYDQYKDAWDTSVVSEIK 142
 QY 61 ----MGEKVRYFHSIKGVRHWIDHFWFLAKYWGKSGSKLYGPRSGADYLDNHRKFAIPC 117
 Db 143 VADRYERVRFFHCYKRGVDVDFIDHPSFLEKVGWGTGKIKYIGPDGTGVDYKQNMRFSLIC 202

Search completed: June 4, 2003, 14:56:01
Job time : 37.3424 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:49:26 ; Search time 11.5821 Seconds
(without alignments)
1653.790 Million cell updates/sec

Title: US-09-980-771A-5

Perfect score: 3370

Sequence: 1 ALDIVVAAEVAFWPWSKTGGL.....SASKTSAKPLVSAATRKSA 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2.6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2.6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1397.5	41.5	609	3	US-08-941-445A-7
2	1360.5	40.4	600	4	US-09-388-743-22
3	1353.5	40.2	533	3	US-08-941-445A-5
4	1342.5	39.8	616	4	US-09-388-743-14
5	1315	39.0	614	4	US-09-388-743-18
6	1314.5	39.0	615	4	US-09-388-743-2
7	902.5	26.8	641	4	US-08-836-567-10
8	882.5	26.2	649	4	US-09-192-909-2
9	881	26.1	671	4	US-09-196-390-2
10	873	25.9	801	4	US-09-388-743-26
11	871	25.8	767	4	US-08-836-567-8
12	861.5	25.6	539	3	US-08-941-445A-21
13	861.5	25.6	583	3	US-08-941-445A-13
14	858	25.5	690	4	US-09-388-743-6
15	845	25.1	558	4	US-08-836-567-6
16	841	25.0	799	4	US-09-196-390-6
17	837	24.8	698	3	US-08-941-445A-11
18	726	21.5	459	4	US-08-836-567-4
19	701.5	20.8	669	3	US-08-941-445A-9
20	580	17.2	477	1	US-07-735-065-2
21	580	17.2	477	1	US-08-469-202-12
22	580	17.2	477	2	US-08-484-434C-12
23	568.5	16.9	677	4	US-08-836-567-2
24	568.5	16.9	1197	4	US-08-836-567-12
25	568.5	16.9	1230	2	US-08-968-542C-35
26	545	16.2	735	4	US-09-115-704-2
27	530.5	15.7	533	4	US-09-388-743-10

28 504 15.0 1674 2 US-08-968-542C-12 Sequence 12, Appl
29 240 7.1 64 2 US-08-470-720-15 Sequence 15, Appl
30 215.5 6.4 79 2 US-08-470-720-13 Sequence 13, Appl
31 145.5 4.3 2035 1 US-08-046-585-5 Sequence 5, Appl
32 145.5 4.3 2035 1 US-08-393-703-5 Sequence 5, Appl
33 145.5 4.3 2035 5 PCT-US93-11721-5 Sequence 5, Appl
34 143.5 4.3 59 2 US-08-470-720-14 Sequence 14, Appl
35 134.5 4.0 1222 2 US-08-682-517-15 Sequence 15, Appl
36 134.5 4.0 1252 2 US-08-682-517-9 Sequence 9, Appl
37 132 3.9 520 4 US-09-000-016-7 Sequence 7, Appl
38 132 3.9 520 4 US-09-514-340-7 Sequence 7, Appl
39 132 3.9 734 4 US-09-000-016-4 Sequence 4, Appl
40 132 3.9 734 4 US-09-514-340-4 Sequence 4, Appl
41 132 3.9 823 4 US-09-000-016-2 Sequence 2, Appl
42 132 3.9 823 4 US-09-514-340-2 Sequence 2, Appl
43 129 3.8 30 2 US-08-470-720-9 Sequence 9, Appl
44 129 3.8 1125 4 US-09-513-783A-152 Sequence 152, App
45 129 3.8 1610 4 US-09-513-783A-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-941-445A-7
; Sequence 7, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P.
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-941-445A-7

Query Match 41.5%; Score 1397.5; DB 3; Length 609;

Best Local Similarity 51.4%; Pred. No. 1.4e-113;

Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;

QY 2 LDIVVAAEVAFWPWSKTGGLDVTGGTGLPTELVKRHRVMTIAPRYDOYDAWDTSVVVDI- 60
DB 83 MNVVFVGAEPWPSKTGGLDVLGLPFPAMAANGHRVMVISPRTQYKDADWTSVVAETK 142

QY 61 ---MGEKVRYSIKKGVHRYWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
DB 143 VADRIYRVRFFHCYKRGVDRFIDPSPLEKVGWGTGKIYGPDTGVGYKDNQMRFSLLC 202
QY 118 KAAIEAARVL-----PFGP---GEDCVFVANDHWSALPVLLAKDEYQPKQFTKAKSVLA 169
DB 203 QAALEAPRLINNNPNFYKGTGYGDEWFCNDWHTGPLASYLKNNYQPNNGIYRNKAVFC 262
QY 170 IHNIAFOGRMWEAEKDKTLPOAAFDKLAFCSDGYAKVYVTEATPMEDEKPLTLGKTYKKI 229
DB 263 IHNISYQGRFAFEDYPELNLSEFRSSEDFIDY-----DTPVEG-----RKI 305
QY 230 NWLKGIIAADKLVTPSPNYATEIAADAAGGVELDTVIRAKGTGIVNGMDIEEWNPKTD 289
DB 306 NNMKAGILEADRVLVSPYYAEELISGIARGCELDNIMELTGTGIVNGMDYSEWDPSKD 365
QY 290 KFLSAPYDONSVYAGAAKAEALQAEGLPVDPTAPLFAFISGRLEBQKGVDDIILAAALPKI 349
DB 366 KYITAKYDATTAEAKALNKEALQAEGLPVDPTAPLFAFISGRLEBQKGVDDIILAAALPKI 425
QY 350 LATPKVQIAILGTGKAAAEKLVNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVPSRF 409
DB 426 M-OEDVOIIVLLGTGKFKKFKLKSMEEEKYDGVKRAVVKVKNAPLAHMLTAGADFMVPSRF 484
QY 410 EPCGLIQLHAMHYGTVPVVAAGTGLVDTYKGVTFGFMGA--LNDPKLDEADADALAATV 467
DB 485 EPCGLIQLQMGYGTGPCACASTGGLVDTYKGVTFGFMGA--LNDPKLDEADADALAATV 544
QY 468 RRASEVFAGGRYPEMVAICISQDLSWSKPAQKWEGLL-----EYVYKGVGVAATKE 518
DB 545 KRAIKVVGTPAYEEMVRNMDLSNKPQAKNENVL--LGLGVAGSAPGIEGDEIAPLA 602
QY 519 KEIKVP 525
DB 603 KENVAAP 609
RESULT 2
US-09-388-743-22
; Sequence 22, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthesis Polynucleotides and Their
; FILE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Tulipa fosteriana
US-09-388-743-22
Query Match 40.4%; Score 1360.5; DB 4; Length 600;
Best Local Similarity 49.9%; Pred. No. 2.3e-110;
Matches 272; Conservative 77; Mismatches 157; Indels 39; Gaps 9;
QY 2 LDIWMAAEVAPWSKGTGLGDTGGTGLPIELVKGHRVMTIAPRDQYADAWDTSVVVDI- 60
DB 73 MNLVFGTGTGPKTSKGLGDLVGLPPLAARGHRVMTIAPRDQYADAWDTSVVVDI- 132
QY 61 MGEK---VRFHSIKKGVHRYWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
DB 133 VGDKMETVRFHHLKRGVDRVIDHPWFLKVGKTSKLYGPRSGADYLDNHRKRALFC 192
QY 118 KAAIEAARVLPE-----GP-GEDCVFVANDHWSALPVLLAKDEYQPKQFTKAKSVLA 169
DB 193 QAALEAPRLINNNPNFYKGTGYGDEWFCNDWHTGPLASYLKNNYQPNNGIYRNKAVFC 252

QY 170 IHNIAFOGRMWEAEKDKTLPOAAFDKLAFCSDGYAKVYVTEATPMEDEKPLTLGKTYKKI 229
DB 253 IHNMAVQGRFAFEDPFDLNLPLPDTFKSSFFDFDGYTK-----PVKGS---RKI 295
QY 230 NWLKGIIAADKLVTPSPNYATEIAADAAGGVELDTVIRAKGTGIVNGMDIEEWNPKTD 289
DB 296 NNMKAGILEADRVLVSPYYAEELISGIARGCELDNIMELTGTGIVNGMDYSEWDPSKD 355
QY 290 KFLSAPYDONSVYAGAAKAEALQAEGLPVDPTAPLFAFISGRLEBQKGVDDIILAAALPKI 349
DB 356 KEITANYDATMTYKRAKGVVKSAPLAHMLTAGADFMVPSRF 409
QY 350 LATPKVQIAILGTGKAAAEKLVNAIGTKYKRAKGVVKSAPLAHMLTAGADFMVPSRF 409
DB 416 M-DENVQIIVLLGTGKFKKFKLKSMEEEKYDGVKRAVVKVKNAPLAHMLTAGADFMVPSRF 474
QY 410 EPCGLIQLHAMHYGTVPVVAAGTGLVDTYKGVTFGFMGA--LNDPKLDEADADALAATV 467
DB 475 EPCGLIQLQMGYGTGPCACASTGGLVDTYKGVTFGFMGA--LNDPKLDEADADALAATV 534
QY 468 RRASEVFAGGRYPEMVAICISQDLSWSKPAQKWEGLL-----EYVYKGVGVAATKE 520
DB 535 KRAIKVVGTPAYEEMVRNMDLSNKPQAKNENVL--LGLGVAGSAPGIEGDEIAPLA 594
QY 521 EIKVP 525
DB 595 NVAAP 599
RESULT 3
US-08-941-445A-5
; Sequence 5, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/941.445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 533 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-941-445A-5


```

QY 170 IHNTAOGRWEEAFKDTKLPOAFAFDKLAISDGYAKVYTEATPMEEDEKPLLTGKYTKI 222
      ||||:||||      ||:      || |||      |:|      ||
Db 268 IHNTSYOGRFSFSPDFEFLNLPENFKSFSFIDGYNK-----PVKG---MKI 310
QY 230 NWLKGGLIIADKLVTSFNPVATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEEWNPKTD 289
      ||||:||||      ||:      |||||      |:| |||||      |||||
Db 311 NWMKAGILESDFVTFSFYTAQELLSGEERGVELDNILRVTSITGIVNGMDVNEWNPITD 370
QY 290 KFLSAPYDQNSVYAGKAAAKEALQAEILGLPVDPTAPLFAFICRLEEQQGVDIILALPKI 349
      |:|      |:|      |||||      |      |      |||||      |:| |:| |:|
Db 371 KYISVNYDAKVPMEAKPLNKEALQAESWLACRQGHPCNCIHRLEEQQGSDIILASIPET 430
QY 350 LATPKVOJAILGTGKAAYEKVLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMLVPSRF 409
Db 431 M-DENVQLIILGTGKKEMENOLESEEMEPFPOKVRAMKFNAPLAHOMTAGADIIIVPSRF 489
QY 410 EPGGLIOLHAMHYCTVPVVASTGGVLDPVKGVTFGHMGALNP--DKLDEADADALAATV 463
Db 490 EPGGLIOLQMOYGTGPSACSTSGGLVDIVKEGKTGFHMGPTSAECEVVDLSVKKVVITV 549
QY 468 KRASEVPAGGRYPPEMVANCISODISWSKPAOKWEGLLLEEVYVGKGVATAKK----EETK 523
      |:|      |:|      |:| |||||      |:|      |:|      |:|      |:|
Db 550 KRALKVITGTPAFEDMIKMKMAQDLISWKGPAKNWEOVLNML-----GVAGSEPGYDGEET- 603
QY 524 VPVAEK 529
Db 604 YPLAKE 609

RESULT 6
US-09-388-743-2
; Sequence 2, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Curcuma zedoaria
US-09-388-743-2

```

```

289 DKLSAPYDONSYYAGKAAKEALQAFELGLPVDPTAPLEAFICRLEEOQGVDIILAALPK 348
371 DKYITANYDATTWEAKPLNKEALQAEVLGPNVKIPVIAFICRLEEQGSDILAELAIKP 430
349 ILATPKVQIAILGTGKAAVEKLVNAIGTKYKRAKGVVXKFSAPLAHMLTAGADMVLVPSR 408
431 FF-DQDVQVIVLGTGKKLERQLALLEDEPDKFRAHMKFNIPLAHGIMAGADILVIPS 489
409 FEPCLLIQLHAMHYGIVPVVASTGGGLVDIVKEGVTGFHMG--ALNDPKLDEADADALAAT 466
490 FEPCCGLTQLOCMRYGTPSMCTTTGGGLVDIVKEGVTGFHMGPFVSVECDIADADVZKIVEA 549
467 VRASEVFAAGGRYPPEMVANCISODLSWSKPAQKWEGLL-----EEVYVYKGGVATAK 518
550 VKRALMVGTPFAEEMTQNCMAQDFSWKKGPAKEWEKFEKLLSLGLESGEACIEGE-EVAPLA 608
519 KEEKIVP 525
609 KENVATP 615

RESULT 7
US-08-836-567-10
; Sequence 10, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-567-10

```



```
QY 3 DIVVAAEAPWPKTGLGVDVGTGLPIELVKRGRHVRMTIAPRY-----DOYADAWDT5 55
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
132 NILVTAAPYKTKGLGVDVGTGLPMAAARGHRVMPVSPRYLNGSPSEKYNAYAVDLD 191
QY 56 V--VVDIMG--EKVYFHSIKKGRHVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHK 111
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
192 VRATVHCFGDAQAEVAFHEYRAGVDWVFDHSSVC-----RPGUP-YGDIYGA-FGDNQF 244
QY 112 RFALFCKAAIEAARVLPFGP---GEDCVFVANDHWSALVPVLLKDEYQPKGQFTKAKSVL 168
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
245 RFTILSHAACEAPLVLPGLGFTYGEKCLFLANDWHAALVPLLAAKYRPGYVKDARSIV 304
QY 169 AIHNIAPQGRWEEAFKDTLPQAAFDKLAFSOGYAKVYVTEATPMEDEKPLTGKTKYK 228
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
305 AIHNIHQVEPAPVTNNLGLPPQWYGAV---EWIPTWARAHALD-----TGET--- 351
QY 229 INWLKGGITAAADKLVTSPNYATEIAADAAGGVDELDTVI--RAKGIEGIVNGMDIEBWP 286
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
352 VNVLKGAIAVADRILVTSOGYSWEIIT-PEGGYCLHELSSRQSVLNGITNGIDVNDWP 410
QY 287 KTDKFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFTRLEEQKGVDIILAA 346
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
411 STDEHLASHYSINDL-SGKVCQCKTDLQKELGLPIRDCPLIGFTGRLDYQKGVDIILSAI 469
QY 347 PKILATPKVQIAILGTGKAAYEKLVAIGTKYKRAKGVVYKFSAPLAHMLTAGADFMVLP 406
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
470 PELMQN-DVQVMLGSGEKYEDWHRHTENLFKDKFRAWGVFNVPVSHRITAGCDILMP 528
QY 407 SRPECGLIQLHAMHYGTVPVVAAGTGLVDIVK-----EGV---TGPHMGALNPKLD 456
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
529 SRPECGLNQLYAMRYGTPIVHSTGGLRDTVKDENFYAQEGIGEGTGWTFSPITSEKL- 587
QY 457 EADADALAATVRASEVFAAGRPE-----MVANCISQDLSWSKPAQKWE 501
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
588 ---LDTKLKLA-----GTYTEHKSWEGLMRMGDRDYSWENAAIQYE 627
```

RESULT 8

```
US-09-192-909-2
; Sequence 2, Application US/09192909
; Patent No. 6307124
; GENERAL INFORMATION:
; APPLICANT: Jens Kossmann
; APPLICANT: Claus Froberg
; TITLE OF INVENTION: Nucleic acid molecules encoding soluble
; TITLE OF INVENTION: Starch synthases from maize
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/192,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02527
; FILING DATE: 16-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 196 19 918.2
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, Jr., James F.
; REGISTRATION NUMBER: 27,794
```

```
; REFERENCE/DOCKET NUMBER: GFB-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-96-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 649 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-192-909-2
```

```
Query Match 26.2%; Score 882.5; DB 4; Length 649;
Best Local Similarity 38.4%; Pred. No. 1.5e-68;
Matches 203; Conservative 95; Mismatches 174; Indels 57; Gaps 15;

QY 3 DIVVAAEAPWPKTGLGVDVGTGLPIELVKRGRHVRMTIAPRY-----DOYADAWDT5V 56
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
142 NIVFTGEASPYAKSGGLGVDVGSPLVALAARGHRVMPVMPRYLNGISDKNYANAFYTEK 201
QY 57 VVDIM--GE-KVRYFHSIKKGRHVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHKR 112
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
202 HIRIPCGGEHEVTFEYRDSVDVVDHPSY-----HRPGNLYGDKTGA-FGDNQFR 254
QY 113 FALFCKAAIEAARVLPFGP---GEDCVFVANDHWSALVPVLLKDEYQPKGQFTKAKSVLA 169
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
255 YTLCCYAAACEAPLVLPGLGFTYGEKCLFLANDWHAALVPLLAAKYRPGYVKDARSILV 314
QY 170 IHNIAPQGRWEEAFKDTLPQAAFDKLAFSOGYAKVYVTEATPMEDEKPLTGKTKYK 229
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
315 IHNIHQVEPAPVTNNLGLPPQWYGAV-----VPEWARHRLDKG-----EAV 361
QY 230 NWLKGITAAADKLVTSPNYATEIAADAAGGVDELDTVI--RAKGIEGIVNGMDIEBWP 287
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
362 NELKGAVTADRIVTGSKYSWEVTT-AEGQGLNELLSRKSXSVLNGIDINDWNP 420
QY 288 TDKFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFTRLEEQKGVDIILAA 347
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 TDKCIPCHYSVDL-SGKAKCGALQELGPIRDPVPLIGFTGRLDYQKGVDIILAI 479
QY 348 KILATPKVQIAILGTGKAAYEKLVAIGTKYKRAKGVVYKFSAPLAHMLTAGADFMVLP 407
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
480 DLM-REDVQVMLGSGDPELEDWNRSTESIFDKFRGWGVGFSVPVSHRITAGCDILMP 538
QY 408 RFPECGLIQLHAMHYGTVPVVAAGTGLVDIVK-----EGVTGPHMGALNPKLDEA 458
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
539 REEPCGLNQLYAMQYGTVPVVAAGTGLVDIVENFEGENGEGTGWAFAPLTEN---- 594
QY 459 DADALAATVRASEVFAAGR--YPEMVANCISQDLSWSKPAQKWEGLLE 505
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
595 ---MLWTLRTAISTYREHKSWEGLMKRGSKDFTDWHAAYEQEIFQ 639
```

RESULT 9

```
US-09-196-390-2
; Sequence 2, Application US/09196390
; Patent No. 6307125
; GENERAL INFORMATION:
; APPLICANT: Block, Martina
; APPLICANT: Loiz, Horst
; APPLICANT: Lutticke, Stephanie
; APPLICANT: Walter, Lennart
; APPLICANT: Froberg, Claus
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
; TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
; TITLE OF INVENTION: SYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
```

COUNTRY: United States of America
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/196,390
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 196 21 588.9
 FILING DATE: 29-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 196 36 917.7
 FILING DATE: 11-SEP-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP97/02793
 FILING DATE: 28-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley, Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: AGREVO-9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 671 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-196-390-2

Query Match 26.1%; Score 881; DB 4; Length 671;
 Best Local Similarity 35.2%; Pred. No. 2.2e-68;

Matches 237; Conservative 94; Mismatches 225; Indels 118; Gaps 22;

QY 4 IVVVAFAVPWSKTGGLDVTGGLPTLTKVGRHVMYIAPY-----DOYADAWDTSVV 57
 DB 56 IVFTGEMAPYAKSGGLDVGCSLPTALARGHRVWVMPRYLNGSSDKNYAKALYAKH 115
 QY 58 VDIN---GBKRYFHSIKGVHRVWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHRF 113
 DB 116 IKIPCGGSHVETTFHEYRONVDWVVDHP-----SYHRPGS-LYGNFCA-FGDNQF 168
 QY 114 ALFCKAAIEAARVLPGP---GEDCVFVANDHWSALVPVLLKDEYQPKQFTAKSVLAI 170
 DB 169 TLICYAAACEAPLILELGGYLYGQNCMEFVNDHWSALVPVLLAARYPYGYVRSRSLVI 228
 QY 171 HNTAFQGRMWEAFKDTKLPOAADFKLAFSDGYAKVYTEATPMEDEKPPLTGKTKYKIN 230
 DB 229 HNTAHQGEVASTYPDLGLPPENYGALEW-----VPEWARHRLDKG-----EAVN 275
 QY 231 WLKGGIIAADKLVTVSPNYATEIAADAAGVVELDTVI--RAKGIEGVINGMDIEWNPKT 288
 DB 276 FLKAVVTAIRIVTVSGSYWEVTT-AEGQGLNELLSRKSVLNGIVNGIDINDWNPPT 334
 QY 289 DKLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFIEGLEQKGVDIILALPK 348
 DB 335 DKCLPHYSVDOL-SGKAKCAEALQKELGLPVRDVPDLTIGFIRLDYQKGLDILTKMAIPE 393
 QY 349 ILATPKVQVIAILGTGKAAEKLVAIGTKYKRAKGVYKFSAPLAHMLTAGADPMLVPSR 408
 DB 394 LM-REDYQFVNLGSDPIFGWMBRSTESSYKDKFRGWGVFSVPVSHRITAGCDILLMP 452
 QY 409 FEPGCLIQHMHVYGVVAVASTGGIVDTVK-----EGVTGFMGALNPDKLEAD 459
 DB 453 FEPGCLNQLYAMQGTVPVYVHGTGGLRDTVETENPFKAGKEEGTGWAFSPLTVDKMLWA- 511
 QY 460 ADALAAVTRASEVAFAGRYPEMVANCISQDLSNKSAPQAKWEGLEEYVYKGVATAKK 519

DB 512 -----LRTAMSTFRE-----HKPS--WEGLM-----KR 532
 QY 520 EEIKVPVAKIPGDLPAVSYPANTLKPVSASVEGNGAAAPKVGTTPAMGAWRATTPSGP 579
 DB 533 GMTKDHTWDHAPSSSTSRSSSGPSWNTPTSC-----RRLGLSRKCESPSAL 577
 QY 580 SPAAT---PKVTYTKPALPATAPKTAGLK-LAGPASTVSTSENGAASNGNGASASK 635
 DB 578 KTSSSFRGPEGYPCITLRCPATVESQCACALLWFAG-----SRTYDGA-----AAAVT 625
 QY 636 TSAAKPLVSAATR 649
 DB 626 AGGROLQFWGIRK 639
 RESULT 10
 US-09-388-743-26
 ; Sequence 26, Application US/09388743
 ; Patent No. 6423886
 ; GENERAL INFORMATION:
 ; APPLICANT: Singletary, George
 ; APPLICANT: Zhou, Lan
 ; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
 ; TITLE OF INVENTION: Use in the Production of New Starches
 ; FILE REFERENCE: 1144
 ; CURRENT APPLICATION NUMBER: US/09/388,743
 ; CURRENT FILING DATE: 1999-09-02
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 26
 ; LENGTH: 801
 ; TYPE: PRT
 ; ORGANISM: Typha latifolia
 ; ORGANISM: Typha latifolia
 ; US-09-388-743-26

Query Match 25.9%; Score 873; DB 4; Length 801;
 Best Local Similarity 38.9%; Pred. No. 1.5e-67;

Matches 211; Conservative 79; Mismatches 166; Indels 86; Gaps 16;

QY 2 LDIVWAAEAPWSKTGGLDVTGGLPTLTKVGRHVMYIAPYDQYADAWDTSV--VVD 59
 DB 226 MNIIVAAECAPWSKTGGLDVGAGALPKALARGHRVWVAPRYNAEPODVGKYYK 285
 QY 60 IMGP--KVRTPHSIKGVHRVWIDHPWFLAKVWGKTGSKLY-GPRSGADYLDNHRALF 116
 DB 286 VHGDMEVTVTHAYIDGVDFVMDSPDFRHR-----GNRIYEGNR-----VDILKRMILF 335
 QY 117 CKAIEAARVL-----FGCEDCVFVANDHWSALVPVLLKDEYQPKQFTAKSVLAIH 171
 DB 336 CKAIEAARVL-----FGCEDCVFVANDHWSALVPVLLKDEYQPKQFTAKSVLAIH 394
 QY 172 NIAFGQRMWEAFKDTKLPOAADFKLAFSDGYAKVYTEATPMEDEKPPLTGKTKYKINW 231
 DB 395 NIAHQGRGPDVDFKVPGLPDHLYDLFLYD-----PVGG-----EHLNI 433
 QY 232 LKGGIIAADKLVTVSPNYATEIAADAAGVVELDTVI--IRGIVNGMDIEWNPKT 289
 DB 434 FAAGLKTADRVTVVSHGYAMELKT-SEGQGLNELLSRKSVLNGIVNGIDAKWSEF 492
 QY 290 KFLSAP---YDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFIEGLEQKGVDIILAA 345
 DB 493 VHLXSDGTYNSLDTLEMGKPVCKAALQREVGLPVRNVPIATFIRLDHKGVDLIAEA 552
 QY 346 LPKTLATPKVQVIAILGTGKAAEKLVAIGTKYKRAKGVYKFSAPLAHMLTAGADPMLV 405
 DB 553 MPWIV-SHDVQVWVMLGTGRDLENLLRNFEQGRDKVRAWVAFSVKMAHRTITAGADILMM 611
 QY 406 PSREPCGLIQHMHVYGVVAVASTGGIVDTVK-----EGVTGFMGALNPDKLEADALAA 465
 DB 612 PSREPCGLNQLYAMQGTVPVYVHGTGGLRDTVETENPFKAGKEEGTGWAFSPLTVDKMLWA- 657
 QY 466 TVRRASEVAFAGRYPEMVANCISQDLSNKSAPQAKWEGLEEYVYKGVATAKK 507

Db 658 TFDRAE-----AGKLIHALNCLNTYWNKDSWKGLQTRGMQDLSWDRRAQQYEDVLVA 713
QY 508 VY 509
Db 714 KY 715
RESULT 11
US-08-836-567-8
; Sequence 8, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossman, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 767 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-567-8
Query Match 25.8%; Score 871; DB 4; Length 767;
Best Local Similarity 39.7%; Pred. No. 2e-67;
Matches 210; Conservative 78; Mismatches 181; Indels 60; Gaps 14;
QY 2 LDIWVAEAPWPSKGTGLDVTGGPLIELVKRHRVMTIAPRYDOYADAWTSV---V 57
Db 276 MNILVASCAPWSTKGLGVDVAGALPKALARHGRVWVAPRIDNYPEQSGVPRKIYK 335
QY 58 VDMGKRYFHSIKKGVHRVWIDHPWFLAKYWGKTSKLYGPRSGADYLDNKHKRALFC 117
Db 336 VDGQDVETVYFOAFIDGVDFEID-----SHMFRHIGNNIY---GGNRVDILKRWLFC 386
QY 118 KAAIEARVLP-----FGGECVCFVANDWHSALVPVLKDEYQPKGQTKAKSVLAHIN 172
Db 387 KAAIEVPWPCGGVYCGDG- NLVFTANDWHTALLFVYLKAYYRDNIMNYTRSVLVIHN 445
QY 173 IAFQGRMWEAFKDKLQPAADFADKLAFSQYAKVYTEATPMEDEKPLTGKTKKINWL 232

Db 446 IAHQGRGFLEDFSYVDLPPHYMDPFKLYD-----PVGGEHF---NIF 484
QY 233 KGGTIAADKLVTVSPNYATEIAADAAGVELDVTIRAKG--IEGIVMGMDTEENPKTDK 290
Db 485 AAGLKTADRVVTVSHGYSWELKT-SQGGWGLHQIINENDWKLOGIVNGIDTKWNPELD 543
QY 291 FLSAP----YDQNSVYAGKAAKAEALQAEGLPVDPTAPLFAFTGRLEEKQGVDTIIAAL 346
Db 544 HLQSDGYMNSLDTLQTKPOCKAALQKELGLPVRDDVPLIGFIRGLDPQKGVDLIAFAS 603
QY 347 PKILATPKVQITAILGTGKAAEYKLVNAIGTKYKGRAGVYKFSAPLAHMLTAGADFMVLP 406
Db 604 AMMG-QDVQLVMLGTGRRDLEQMLRFQECQHNKIRGWGFSVKTSRITAGADILLMP 662
QY 407 SRPEPCGLIOLHAMHYGTVPVASTGGIVDTVK-----EGVTGFHMGALNPKDLDEADA 460
Db 663 SRPEPCGLNQLYAMKYGTIPVHVAGGLRDTVPQDFPFNESGLGWTFSRAEASQLIHAG 722
QY 461 DATAATVRRASEVFAAGRYPEMVANCISQDLSWSKPAQKWEGLEEYVY 509
Db 723 NCL-LTYREYKKSWEG-----IOTRCMTQDLSWDAQAQNYEEVLIAAKY 765
RESULT 12
US-08-941-445A-21
; Sequence 21, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 539 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-941-445A-21
Query Match 25.6%; Score 861.5; DB 3; Length 539;
Best Local Similarity 40.8%; Pred. No. 7.9e-67;
Matches 194; Conservative 81; Mismatches 154; Indels 47; Gaps 13;
QY 4 IYVVAEAPWPSKGTGLDVTGGPLIELVKRHRVMTIAPRY-----DOYADAWTSV 57

Db 51 IVFVTGEASPYAKSGGLGDCVGLPVALAARGHRVVMVMPRYLNGTSDKNYANAFYTEKH 110
QY 58 VDIM---GE-KVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKF 113
Db 111 IRIPCFCGGEHEVTFHEYRDSYDVWVFDHPSY-----HRPGLNLYGDKFKA-FGDNQFRI 163
QY 114 ALFCAATEAARVLPFGP---GEDCVFVANDHNSALVPVLLKDEYQPKQFTKAKSVLAI 170
Db 164 TLLCYAACEAPLILELGGYIYQNCMFVVDNDHNSALVPVLLAARYPYGVYKDSRSILVI 223
QY 171 HNAIFGGRWEAEAFKDTKLPOAFAFKLAFSDGYAKVYVTEATPMEDEKPLTGKTYKKIN 230
Db 224 HNLHOGVPEASTYDGLPPEWYGALEW-----VFPWARHRLDKG-----EAVN 270
QY 231 WLKGGIIAADKLVTSVSNYATEIAADAAGGVLDTVI--RANGIEGIVNGMDEEWNPKT 288
Db 271 FLKGAVVADRIVTVSKGYSWEVTT-AGGQGLNELLSSRKSVLNGVINGIDINDNPNAT 329
QY 289 DKFLSAPYDQNSVYAKAAKAEALQAEGLPVDPTAPLFAFIRGLEEQKGVDIILALPK 348
Db 330 KCIPCCHYSVDL-SGKAKCKGALQELGLPIRPDVPFLIGFIRGLDYQKGDILQIIPD 388
QY 349 ILATPKVQIAILGTGKAAEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADFMVLPSP 408
Db 389 LM-REDVQFVMLGSDPDELDWNRSTESIFKDKFRGWGFSVPVSHRITAGCDILLMPSP 447
QY 409 FEPCGLIQLHAMHYGTPVVPVASTGGGLVDTVK-----EGVTGFHMGALNPDKL 455
Db 448 FEPCGLNQLYAMQYGVVPHATGGLDRDVENENPFGEQGTGWAFAPLTENN 503

RESULT 13

US-08-941-445A-13
; Sequence 13, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-941-445A-13

Query Match 25.6%; Score 861.5; DB 3; Length 583;
Best Local Similarity 40.8%; Pred. No. 8.9e-67;
Matches 194; Conservative 81; Mismatches 154; Indels 47; Gaps 13;
QY 4 IYVAAEAVPWSKTSGLGVDVGTGLPIELVKRHRVMTIAPRY-----DOYADAWDTSVV 57
Db 95 IVFVTGEASPYAKSGGLGDCVGLPVALAARGHRVVMVMPRYLNGTSDKNYANAFYTEKH 154
QY 58 VDIM---GE-KVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKF 113
Db 155 IRIPCFCGGEHEVTFHEYRDSYDVWVFDHPSY-----HRPGLNLYGDKFKA-FGDNQFRI 207
QY 114 ALFCAATEAARVLPFGP---GEDCVFVANDHNSALVPVLLKDEYQPKQFTKAKSVLAI 170
Db 208 TLLCYAACEAPLILELGGYIYQNCMFVVDNDHNSALVPVLLAARYPYGVYKDSRSILVI 267
QY 171 HNAIFGGRWEAEAFKDTKLPOAFAFKLAFSDGYAKVYVTEATPMEDEKPLTGKTYKKIN 230
Db 268 HNLHOGVPEASTYDGLPPEWYGALEW-----VFPWARHRLDKG-----EAVN 314
QY 231 WLKGGIIAADKLVTSVSNYATEIAADAAGGVLDTVI--RANGIEGIVNGMDEEWNPKT 288
Db 315 FLKGAVVADRIVTVSKGYSWEVTT-AGGQGLNELLSSRKSVLNGVINGIDINDNPNAT 373
QY 289 DKFLSAPYDQNSVYAKAAKAEALQAEGLPVDPTAPLFAFIRGLEEQKGVDIILALPK 348
Db 374 KCIPCCHYSVDL-SGKAKCKGALQELGLPIRPDVPFLIGFIRGLDYQKGDILQIIPD 432
QY 349 ILATPKVQIAILGTGKAAEKLVAIGTKYKRAKGVVKSAPLAHMLTAGADFMVLPSP 408
Db 433 LM-REDVQFVMLGSDPDELDWNRSTESIFKDKFRGWGFSVPVSHRITAGCDILLMPSP 491
QY 409 FEPCGLIQLHAMHYGTPVVPVASTGGGLVDTVK-----EGVTGFHMGALNPDKL 455
Db 492 FEPCGLNQLYAMQYGVVPHATGGLDRDVENENPFGEQGTGWAFAPLTENN 547

RESULT 14

US-09-388-743-6
; Sequence 6, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthese Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Curcuma zedoaria
US-09-388-743-6

Query Match 25.5%; Score 858; DB 4; Length 690;
Best Local Similarity 39.0%; Pred. No. 2.4e-66;
Matches 208; Conservative 80; Mismatches 176; Indels 70; Gaps 15;
QY 2 LDIVVAAEAVPWSKTSGLGVDVGTGLPIELVKRHRVMTIAPRYDYQADAWDTSVV---- 57
Db 199 MNILVAAECAPWSKTSGLGVDVGTGLPIELVKRHRVMTIAPRYDYQADAWDTSVV---- 258
QY 58 VDIMEKVRVYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKFALFC 117
Db 259 VDGQDMEIKYTHYIIDSVDVFDISP-----IFRHINDIY----GGNVDILKRWVLC 309
QY 118 KAAIEAARVLP-----FGPDCVYFVANDHNSALVPVLLKDEYQPKQFTKAKSVLAIHN 172
Db 310 KAAVEVPHVPCGGFCYGDG-NLVFIANDWETSLLPVYLKACFRDGLMTYARCLIVHN 368

```

QY 173 IAFQGRWREAEKDTKLPOAAFDKLAESDGYAKVYTEATPMEDEKPPILGKTYKKINWL 232
Db 369 IAHQGRPLDDFSDVLDHHDHDSFRLLD-----PVGGEHF---NIF 407
QY 233 KGGIITAADKLVTSPNYATEIAADAAGVVELDTPVIRA--KGIEGIVNGMDIEBWNPKTDK 290
Db 408 AAGIRAADRVTVSHGYANFKLT-SRGGWGLHFIINECHWKHFGIYNGIDTSHWNPKFDA 466
QY 291 FLSAP-----YDONSVTAGKAAKEALQAEGLPVDPTAPLFAFGRLEEQKGYDIIAAL 346
Db 467 HLNSDGYTFTLTLEMGRAQCAKALQREFGLPVRDDVPTLAFIQRDLHQGDILTAEM 526
QY 347 PKILATPKVOIALGTGKAAEKLVAIGTKYGRAGVYKVSAPLAHMLTAGADPMLVP 406
Db 527 -HWLVQDQIILMLGGRPDLEMLRFREREHKGVRGWGVSVMMAHRIITAGADALLMP 585
QY 407 SRFEPCGLIQLHAMHYGTVPVVAAGVVELDTPVIRA--KGIEGIVNGMDIEBWNPKTDK 290
Db 586 SRFEPCGLIQLHAMHYGTVPVVAAGVVELDTPVIRA--KGIEGIVNGMDIEBWNPKTDK 290
QY 463 LAA-----TVRRASEVAGRYPEMVAANCISQDLSWSKPAQKWEGLLEEVY 509
Db 640 MIVALGHCLNTYRNKESVGLQKRGMM-----QDLSWSAABHYEKLVAARY 556

RESULT 15
US-08-836-567-6
; Sequence 6, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 558 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

US-08-836-567-6

Query Match 25.1%; Score 845; DB 4; Length 558;
 Best Local Similarity 39.1%; Pred. No. 2.3e-65;
 Matches 207; Conservative 78; Mismatches 184; Indels 60; Gaps 14;

```

QY 2 LDIVMAAEVAPSKSGGLGDTGGPLPIELVKGHRVMTIAPRYDOYADWDTSV----V 57
Db 67 MNILVASECAPSKSGGLGDTGGPLKALARRGHRVMTIAPRYDOYADWDTSV----V 126
QY 58 VDLMGKVRVYFHSIKKGVHVDHPWFLAKVWCKTGSKLYGSPSGADYLDNHRKFRALFC 117
Db 127 VQGDQEVITYFQAFIDGVDFVFD-----SHMERHGNINNY-----GGRVVDILKRMVLF 177
QY 118 KAAIEAARVLP-----FGPCEDCVFVANDHSAIPLVLLKDEYQPKQOFTKAKSVLAHN 172
Db 178 KAAIEVPHVPCGVCYGDG-NLVFIANDWHTALLPVLYKAYYEDNGIMNYTSLVLIHN 236
QY 173 IAFQGRWREAEKDTKLPOAAFDKLAESDGYAKVYTEATPMEDEKPPILGKTYKKINWL 232
Db 237 IAHQGRPLDDFSDVLDHHDHDSFRLLD-----PVGGEHF---NIF 275
QY 233 KGGIITAADKLVTSPNYATEIAADAAGVVELDTPVIRA--KGIEGIVNGMDIEBWNPKTDK 290
Db 276 AAGKTADRVTVSHGYANFKLT-SRGGWGLHFIINECHWKHFGIYNGIDTSHWNPKFDA 466
QY 291 FLSAP-----YDONSVTAGKAAKEALQAEGLPVDPTAPLFAFGRLEEQKGYDIIAAL 346
Db 335 HLQSDGYMNYSLDTLQTKRQCKRAALQKELGLPVRDDVPTLAFIQRDLHQGDILTAEM 394
QY 347 PKILATPKVOIALGTGKAAEKLVAIGTKYGRAGVYKVSAPLAHMLTAGADPMLVP 406
Db 395 AWMNG-QDVLVMLGTGRDLQRLQFECQHNDRKIRGWVGFVSKTSHRITAGADILLMP 453
QY 407 SRFEPCGLIQLHAMHYGTVPVVAAGVVELDTPVIRA--KGIEGIVNGMDIEBWNPKTDK 290
Db 454 SRFEALRLNQLYAMKYGTIPVHVAVGLRDTVQFPDFNBSGLGWTFSRAESQLIHAG 513
QY 461 DALATVRRASEVAGRYPEMVAANCISQDLSWSKPAQKWEGLLEEVY 509
Db 514 NCL-LTVREYKKSWEG-----IQTRCMTQDLSWDAQAQNYEVLIAKY 556

```

Search completed: June 4, 2003, 14:58:40
 Job time : 16.5821 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:56:21 ; Search time 20.1047 Seconds
(without alignments)
3342.965 Million cell updates/sec

Title: US-09-980-771a-5
Perfect score: 3370
Sequence: 1 ALDIYVAAEVPWKTGGL.....SASKTSAARPLVNAATRKSA 651

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB_PEP.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB_PEP.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCIU8_PUBCOMB_PEP.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_PEP.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_PEP.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB_PEP.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1450.5	43.0	636	9	US-10-138-075-4
2	1433.5	42.5	609	9	US-10-138-075-2
3	1379	40.9	599	9	US-10-138-075-5
4	881	26.1	671	10	US-09-952-677-2
5	841	25.0	799	10	US-09-952-677-6
6	555	16.5	915	9	US-10-163-214-6
7	549	16.3	914	9	US-10-163-214-12
8	545	16.2	909	9	US-10-163-214-2
9	537	15.9	874	9	US-10-163-214-13
10	410.5	12.2	474	12	US-10-007-693-99
11	402.5	11.9	476	12	US-10-007-693-69
12	385.5	11.4	293	9	US-10-163-214-10
13	215.5	6.1	117	10	US-09-739-438-2
14	206	6.1	409	9	US-09-738-626-4738
15	189	5.6	381	9	US-09-738-626-5896
16	164	4.9	143	10	US-09-739-438-4
17	155.5	4.6	191	10	US-09-924-358-22
18	155.5	4.6	418	9	US-09-738-626-3951
19	136.5	4.1	385	10	US-09-767-041-18

20	135	4.0	2993	9	US-09-738-626-6239	Sequence 6239, Ap
21	134.5	4.0	1222	10	US-09-137-531-15	Sequence 15, Appl
22	134.5	4.0	1252	10	US-09-137-531-9	Sequence 9, Appl
23	129	3.8	1125	9	US-10-100-957A-152	Sequence 152, Appl
24	129	3.8	1610	9	US-10-100-957A-22	Sequence 22, Appl
25	128	3.8	2910	9	US-10-124-800-2	Sequence 16, Appl
26	126	3.7	387	9	US-09-738-626-3890	Sequence 3890, Ap
27	125.5	3.7	398	10	US-09-934-899-16	Sequence 36, Appl
28	125.5	3.7	398	10	US-09-934-868-36	Sequence 40, Appl
29	124.5	3.7	1704	9	US-09-991-262-40	Sequence 6655, Ap
30	124	3.7	379	9	US-09-738-626-6655	Sequence 88, Appl
31	124	3.7	1461	9	US-10-021-955-88	Sequence 4025, Ap
32	123.5	3.7	413	9	US-09-738-626-4025	Sequence 3, Appl
33	123	3.6	1528	9	US-09-945-917-3	Sequence 4, Appl
34	123	3.6	1583	9	US-09-945-917-4	Sequence 116, Appl
35	121	3.6	339	9	US-09-847-208-116	Sequence 5277, Ap
36	118.5	3.5	372	10	US-09-815-242-5277	Sequence 12605, A
37	118.5	3.5	384	10	US-09-815-242-12605	Sequence 2, Appl
38	118	3.5	267	10	US-09-852-555-2	Sequence 147, App
39	118	3.5	333	9	US-09-847-208-147	Sequence 69, Appl
40	118	3.5	1463	9	US-09-971-536-69	Sequence 5590, Ap
41	117.5	3.5	636	9	US-09-738-626-5590	Sequence 1, Appl
42	117	3.5	3241	10	US-09-841-786-1	Sequence 33, Appl
43	117	3.5	3739	9	US-09-860-846-33	Sequence 33, Appl
44	117	3.5	3739	9	US-09-988-384B-33	Sequence 33, Appl
45	117	3.5	3739	9	US-09-836-821-33	

ALIGNMENTS

RESULT 1

US-10-138-075-4
; Sequence 4, Application US/10138075
; Publication No. US20030087369A1
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Orozco, Emil M.
; TITLE OF INVENTION: Granule-Bound Starch Synthase
; FILE REFERENCE: BB1474 NA
; CURRENT APPLICATION NUMBER: US/10138, 075
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/288,315
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Glycine max
US-10-138-075-4

QY	2	LDIVVAAEVPWKTGGLGDTYGGLPPIELVKRGHVMITAPRYDOYADADTSSVVVDI-	60
Db	106	MTFIIGTVEAPWCKTGGGLGDLVGLPPALGFGHRVMTIVPRYDOYKDAWDTSSVVEVK	165
QY	61	---MGEKVFYFHSIKKGVHVRWIDHPWFLAKYVWGKGLYGRSGADYLDNKKFALPC	117
Db	166	VGDRTEKVFYFHCYKRGVDVDFVDFHFWFLKGVKGTGQKLYGTTGNDYEDNQLRESLFC	225
QY	118	KAALEAARVLPF-----GP-GEDCVFVANDWHSALVFLKDEYQPKQGTAKKSVLA	169
Db	226	QAALAEAPRVLSNSSKYSFGPGVEDVIFVANDWHTALIPCYLKSMYQSRGIYTNARVFC	285
QY	170	INIAFOGRMWEAEKDKLPQAAFDKLAFSOGYAKVYVTEATPMFEDEKPPITGTYKKI	229

Db 355 DKVISYKYNATTVAEARLNKEILQAEVGLPVDSSIPVIVFIGNLEBQKSGDILLAAIPE 414
QY 349 ILATPKVQIATLGTGAAYEKLYNAITGTYKGRAGKGVVVFSAPLAHLMTAGADFMVPSR 408
Db 415 FL-EENVQIIVLTGTRKKMEELMLLEAKYPQNGRIAKENVPLAHMFACANFVPSR 473
QY 409 FEPGGLIQLHAMHYGVVPPVASTGGVLDVTKYEGVTGFHMGALNP--DKLDEADADALAT 466
Db 474 FEPGGLIQLGMRIGYVIPCSTSGGLVDVTVSEGVTFHMGSNFVFEFVDPADVAASN 533
QY 467 VRRASEVAGGRYPFEMVANCISODLSWSKPAQKWEGLLEEVYKKG-----GVA 515
Db 534 VTRALQYKTPPSHAMVQNCMAQDLSKKGPAKWK-----EHALGLGVESQPGIEGEIA 589
QY 516 TAKKEELKVP 525
Db 590 PLAKQNVATP 599

RESULT 4

US-09-952-677-2
; Sequence 2, Application US/09952677
; Patent No. US20020138876A1
; GENERAL INFORMATION:
; APPLICANT: Block, Martina
; Lorz, Horst
; Lutticke, Stephanie
; Walter, Lennart
; Froberg, Claus
; Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
; FROM WHEAT WHICH ARE INVOLVED IN STARCH
; SYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,677
; FILING DATE: 14-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,390
; FILING DATE: 19-No. US20020138876A1-1998
; APPLICATION NUMBER: DE 196 21 588.9
; FILING DATE: 29-MAY-1996
; APPLICATION NUMBER: DE 196 36 917.7
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: PCT/EP97/02793
; FILING DATE: 28-MAY-1997

ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-952-677-2

Query Match 26.1%; Score 881; DB 10; Length 671;
Best Local Similarity 35.2%; Pred. No. 1.9e-54;
Matches 237; Conservative 94; Mismatches 225; Indels 118; Gaps 22;
QY 4 IVWVAARVAWSKGGGLDVTGGPLIELVTRGRHVRMTIAPRY-----DQYADAWDTSVV 57
Db 56 IVFTGTGAAPYAKSGGLDVCGLPILAAARGHRVVMVMPRYLNGSSDKNYAKALYATAKH 115
QY 58 VDJM---GKVRVYFHSIKKGVRHVDHDFWFLAKVWGKTSKLYGPRSGADYLDNHRF 113
Db 116 IKPFCFSGSHEVTFEYRDNVWVFDHP-----SYHRFGS-IYGNDFGA-FGDNQF 168
QY 114 ALFCKAAIEAARVLFPFG---GEDCVFVANDHWSALVPVLIKDEYQPKGQFTAKSVLAI 170
Db 169 TLLCYAAACEAPLILELGGYIVGQNCMFVNDHWSALVPVLLAAKYRYPYGYVYRDSRLVI 228
QY 171 HNTAFQGRWEEAFKDTKLQAAFPDKLAFSDGYAKVYTEATPMEDEKPLTGTKYKKN 230
Db 229 HNLHQGVPEASTYPDLGLPPEWYGALEW-----VPEWARHRLDKG-----EAVN 275
QY 231 WLKGGIIAADKLVTVSPNYATEIAADAAGGVVELDTVI--RAKGIEGIVNGMDIEEWPKT 288
Db 276 FLKGVVTVADRVTVSGYISWEVIT-AEGGQGLNELLSSKSVLNGVINGIDINDWNP 334
QY 289 DKFLSAPYDQNSYVAGKAAKAEALQAEGLGVDPDTAPLFAFIFIGLEBQKGVDIILAAAPK 348
Db 335 DKCLPHYSVDDL-SGKAKCKAELOKELGLPVREDVPLIGFIGRLDYOKGIDLKMAIPE 393
QY 349 ILATPKVQIATLGTGAAYEKLYNAITGTYKGRAGKGVVVFSAPLAHLMTAGADFMVPSR 408
Db 394 LM-REDVQFVMLSGSDPIFEGWMRSTESSYKDKFRGWGVSPVSHRITAGCDILLMPSR 452
QY 409 FEPGLIQLHAMHYGVVPPVASTGGVLDVTK-----EGVTGFHMGALNPDKDEAD 459
Db 453 FEPGGLNQLYAMQYGVVPPVHGGGLRDTVETFPNFCAGKEGEGTGWAFSLPVDKMLWA- 511
QY 460 ADALATVRRASEVAGGRYPFEMVANCISODLSWSKPAQKWEGLLEEVYKKGAVATAK 519
Db 512 -----LRTAMSTFRE-----HKPS--WEGLM-----KR 532
QY 520 EELKVPVAEKIPGDLPAVSYAPNTLKPVSASVEGNGAAAPKVGTATAMGAWRATTSPGP 579
Db 533 GMTKHTWDHAPSTSSSSGSPSWNTPTSC-----RRGLGRKSCSPSAL 577
QY 580 SPAAT---PKVTITYKPAIPATAPKPTAGLK-LAGEASTTSTSENGAASNGNGNGASASK 635
Db 578 KTSSSSFERGPEGYPCITLRCPTAVESQCACILLWFAQ-----SRTVDGCA-----AAV 625
QY 636 TSAKPLVSAATRK 649
Db 626 ASGGRQLQFWGIRK 639

RESULT 5

US-09-952-677-6
; Sequence 6, Application US/09952677
; Patent No. US20020138876A1
; GENERAL INFORMATION:
; APPLICANT: Block, Martina
; Lorz, Horst
; Lutticke, Stephanie
; Walter, Lennart
; Froberg, Claus
; Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
; FROM WHEAT WHICH ARE INVOLVED IN STARCH
; SYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York


```

US-10-163-214-12
; Sequence 12, Application US/10163214
; Publication No. US20030097688A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-163-214-12

```

Query Match	16.3%	Score 549;	DB 9;	Length 914;
Best Local Similarity	30.8%;	Pred. No. 1.1e-30;		
Matches 169;	Conservative 89;	Mismatches 202;	Indels 88;	Gaps 22;
QY	2	LDIVMAAEAPVAKSKTGGCGDVTGGLPIELVKRGHRVMTIAPYD-QYADAWTSTVVVDI	60	
Db	421	LHIAHTAAEMAPVAKVGGGLADVLSGGKALQKKGHVEILPKYDCMQVDQVSNLKYLDV	480	
QY	61	MGEKVRYFHSIRKGVHRVWIDHPWFLKALVWYKGT--GSKLY--GPR-----SGADYLDNH	110	
Db	481	LVQS--YF-----EGNMFNKNIWGTGVEGLPYVEIEPQHPAMEFFSRAQYGEH	526	
QY	111	---KRFALFCKAAIEAARVLPGPGEDC-VFVANDHWSALVPVLLKDEYKPGQKPTAKS	166	
Db	527	DDFKFSEYSRAALE---LLYOSGKKVDIIHCHDWQTAFAPLYWDVYANLG-FNSARI	581	
QY	167	VLAHNHIAFOGRMWEEAEFKDTKLPOAAFDKLAFCSDGAKVYTEATPWEEDKPP-LTGKT	225	
Db	582	CTCHNFEYQG-----TAPADLAWC-----GLDVEHLDRDPRMRONS	619	
QY	226	YKKNWLKGGIIAADKLVTVSPNYAETIAADAAGGVYELDTVIRAKGIEGIVNGMDEEWN	285	
Db	620	HGRINAKGAVVYSNTVTSPTVYALEVRSEGGRLQDTLKVHSRKFGLINGIDDTWN	679	
QY	286	PKTDRLSAPYDQNSVYACKAAKALQAFGL-L-PVDPTAPLFAFTGRLEEQKGVDIILA	344	
Db	680	PCTDRYLKVQYNAKDL-QGKAANKAALRQNLNASAYPSOPLVGCITRLVQAQGVHLIRH	738	
QY	345	ALPKILATPKVQITAILGTGKAAYEKIVNAIGTKYKGRA-----KGWKFSAPLAHM	395	
Db	739	ATVK-TAELGGQFVLGSSP-----VPEIQREFEGIAHFNQNNNIRLLKLYDDALSHC	791	
QY	396	LTAGADFMLVPSPFFPCGLIQLHAMHYGVVPVYASTGGVLVDV-----KGVTVGFHMGALN	451	
Db	792	ITYAASDMFIVPSIFPCGGLQTAMRYGSPVIRKTKGLGDNVSFYDFDDDETIP---MEVRN	848	
QY	452	PKDLDEADADALAAATVRRASEVFAFGRYGPEMWANCISODL---SWSKPAQKWEGLEEV	507	
Db	849	GFTFVKADEOGLSSAMERAFNCYT--RKPEVWKQLVKQDMTIDFSWDTASQYEDIYQA	906	
QY	508	VYKGGVA 515		
Db	907	VARARAVA 914		

RESULT 8
US-10-163-214-2
; Sequence 2, Application US/10163214
; Publication No. US20030097688A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.

```

; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthese Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 909
; TYPE: PRT
; ORGANISM: zea mays
US-10-163-214-2

Query Match          16.2%; Score 545; DB 9; Length 909;
Best Local Similarity 29.4%; Pred. No.2.le-30;
Matches 159; Conservative 92; Mismatches 199; Indels 90; Gaps 20;

QY      2 LDIVMTAAEYAPWPKSTGGGLDVTGGPIELVKRGRHVMTIAPRYD-QYADAWDTSWVDI 60
Db      416 LHIVHTAAEMAPYAKVGGGLADYISGLGKALQKKGHLVEILPKYDCMQHQNINLKVLDV 475
QY      61 MGEKVRYFHSIKGVYHRVWIDHPFWFLAKYWGKT--GSKLY--GPRSGADLY----- 107
Db      476 -----VVKSYFEGNMFANKIWTGIVEGLPVYFTEPQHPGKFFWRAQYCGEH 521
QY      108 DNHKRALCKAAIEAARVLPFGPGEDC-VFVANDHWSALVPVLKLDYFOPGQFTKAKS 166
Db      522 DDFKRFYSFSRVALE---LLYQSGKKVDIIHCMDWQTAFAPLYWDVYANLG-FNSARI 576
QY      167 VLAIHNAIFQGRMWEAEAKDTKLPOAAFDKLFSDGYAKVYVTEATPMEDEKPLTGKTY 226
Db      577 CFTCHNFEYQG-----IAPQDLAYCGLDVDVHLDLPDR--MRDNSH 615
QY      227 KKNLWKGIIAADKLVTYSPNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEENWP 286
Db      616 GRINVYKGAIVYSNIWTVTSPTYAQEVSRSEGGRLQDTLKVHSSKFFVGLINGLIDTDWNP 675
QY      287 KIDKFLSAPYDQNSYAGKAAKEALQAEGL-PVDPTAPLPAFTAGRLLEEKGVDIILAA 345
Db      676 STDRFLKVOYSANDLY-GKSANKAARLKOLKLASTQASQPLVGCITRLVPQKGVHLIRHA 734
QY      346 LPKILATPKVQIATLGTGKAAE-EKIVNAIGTKYK--GRAKGVVAFSAPLAHMLTAGADF 402
Db      735 IYKTELGG-QFVLGSSPVQHOREFGIADQFQNNNVRLLYDALAHNIFAASDM 793
QY      403 MLVPSRFEPCGLIQLHAMHYGPVYVASTGGLVDT-----VKEGYTGPHMGAL 450
Db      794 FIVPSMFEPCGLTQVMAMRYGSPVVRRTGGLNDSEVFDLDDDETIPMEVRNGFTFL----- 848
QY      451 NPDKLEADADALATVRRASEVFAGGRYPENVMANCISDL-----SWSKPAQKWGLLEE 506
Db      849 ---KADEQD---FGNALERAFNY--HRKPEYWKOLVQKMKIDFSWDTSVSQYEIYQK 900

RESULT 9
US-10-163-214-13
; Sequence 13, Application US/10163214
; Publication No. US20030097688A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Starch Synthese Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08

```

Query Match	11.9%;	Score 402.5;	DB 12;	Length 476;
Best Local Similarity	26.9%;	pred. No. 1.2e-20;		
Matches 150;	Conservative 78;	Mismatches 204;	Indels 125;	Gaps 24;
Qy	4	IVMVAAEVPMSKYGGLDVTGGPIELIVKSGHRVMTIAPRY---	DQYADAWDTSVVVDI	60
Db	3	IVQVAVETPIVKVGGGLDVAASIKELAKG-NDVEVLLPHYPLISKFSS-	-----QV	54
Qy	61	MGEKRVFHSIKKGVHRVWIDHPFLAKVWGKTSKLYGP-	-----RSGAD	105
Db	55	LSERSFYFE-----FLGQQAISAISYSEGLTLTIITLDSQIELFTSTTSV	99	
Qy	106	YLDNH-KRFALECKAAIEAARVLPFGPGCEDCVFVANDWHSAIYPVLLKDEVPQKQFTKA	164	

Query Match 12.28; Score 410.5; DB 12; Length 474;

Db 100 YSENNVVRFSAPAAAA--AAYLQADPAD--IVHLHDWHVGLLAGLLKNLPN-----VHS 151
QY 165 KSVLAHNTAFQGRMEAEAFKTLQQAEDKLAESDGYAKVYATEATPMEDEKPPITGK 224
Db 152 KIYFTIHNFYRG-----YCSSTQILAA-----QIDDFHLSHY-----QLFRDPQTSV 194
QY 225 TYKKINWLKGGIILAADKLVTSYSPNATEIAADAAGGVGLDVIRAKG--TEGIVNGMDIE 282
Db 195 L-----MKGALYCSYIITVSYVQEIINDYS-DYELHDAILARNSVFGIINGDED 247
QY 283 ENPKTKDKFLSAPYD-----QNSVYAGKAAAEALQAEGLPVDPTAPLFAFIRGEEQ 336
Db 248 VNNPKTDPALAVOYDASILLSEPDVLTFTKKEENRAVLVEKLGISD-YFPLICVISRVEE 306
QY 337 KG-----VDIILALPKILATPKVQIAILGTGKAAEYKLVNAIGTKYGRAGK-----VVK 387
Db 307 KGFPEFKEIILHAMESYA-----FILIGTSQ--NEVLLNEFRNLQDCLASSPNIRLILD 359
QY 388 FSAPLAHMLTAGADEMLVPSRFEPCGLIQLHAMHYGTVPVASTGGGLVDTVKEGVTGFHM 447
Db 360 FNDPLARLYAADMICISHRACGLTQLIAMRYGTVPVLRKTGGIADTVIPGVNGFTF 419
QY 448 GALNPKLDEADADALAATVRRASEVFAGGRYPFEMVANCISQDLSSWSKPAQKWGLEEV 507
Db 420 --FDTNNE-----FRAMLSNAV-----TYRQEPDVLNLIESG 453
QY 508 VYKGGGVATAKKEIKV 524
Db 454 MLRASGLDAMAKHYVNL 470

RESULT 12

US-10-163-214-10
; Sequence 10, Application US/10163214
; Publication No. US20030097688A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butier, Karlene H.
; APPLICANT: Thorpe, Cathy
; TITLE OF INVENTION: Starch Synthase Isoform V
; FILE REFERENCE: BB1520 US NA
; CURRENT APPLICATION NUMBER: US/10/163,214
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/297,099
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-163-214-10

Query Match 11.4%; Score 385.5; DB 9; Length 293;
Best Local Similarity 33.0%; Pred. No. 9.5e-20;
Matches 101; Conservative 59; Mismatches 115; Indels 31; Gaps 9;
QY 228 KINWLKGGIILAADKLVTSYSPNATEIAADAAGGVGLDVIRAKGIEGIVNGMDIEENPK 287
Db 1 RINAYKGVVYSNIVTTSPTVALEVRSEGGRLQDTLKVHRSKFLIGLNGIDTDWNP 60
QY 288 TDKEISAPYDQNSVYAGKAAAEALQAEGL-PVDPTAPLFAFIRGEEQKGVDIILAL 346
Db 61 TDRIYLVQVNAKDL-OGKAANAALREQLNASYPSQPLVGCITRLVAQKGVHLIRHAI 119
QY 347 PKILATPKVQIAILGTGKAAEYKLVNAIGTKYGRAGK-----KGVVKSAPLAHMLT 397
Db 120 YK-TRELGGQFVLLGSSP-----VPEIQREFEGLADHPQNNNNRILIKYDDALSHCIY 172
QY 398 AGADEMLVPSRFEPCGLIQLHAMHYGTVPVASTGGGLVDTV-----KEGVTGFHMGALNPD 453
Db 173 AASDMFVPSIEPCGLTQMIAMRYGSPVIRKVTGGLNDSVDFDDEITP---MEVRNGF 229

QY 454 KLDEADADALAATVRRASEVFAGGRYPFEMVANCISQDL-----SWSKPAQKWGLEEVVY 509
Db 230 TEVKADBEQGLSSAMERAFNCYT--RKPEVWKQLVQKDMTIDFSWDTASQYEDIYQKAYA 287
QY 510 KKGVA 515
Db 288 RARAVA 293

RESULT 13

US-09-739-438-2
; Sequence 2, Application US/09739438
; Patent No. US20020029394A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Thorpe, Cathy
; TITLE OF INVENTION: Homologs of Starch Synthase DUI
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/739,438
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/171514
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-739-438-2

Query Match 6.4%; Score 215.5; DB 10; Length 117;
Best Local Similarity 46.6%; Pred. No. 3.2e-08;
Matches 41; Conservative 17; Mismatches 25; Indels 5; Gaps 1;

QY 356 QIALGTG-----KAAEYKLVNAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSRFE 410
Db 8 QVVLGSA PDHRIQDFTNLASKLHGEGHGRVLCCLTYDEPLSHLIYAGADFILVPSMFE 67
QY 411 PCGLIQLHAMHYGTVPVASTGGGLVDTV 438
Db 68 PCGLTQLTAMRYGSIPIVKTGGIYDTV 95

RESULT 14

US-09-738-626-4738
; Sequence 4738, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4738

```

138  DB      GTIEDVLTYSQYLLRREFKSAFGSHPTFEHLPSGVDDKRRFTPAT-----PED----- 180
305  QY      KAAAKEALQAEGLGVDPDPTAPLPAFTGRLEEQKGVDIILALPKILAT-PKVOITAILCTG 363
185  DB      ----KSATRKKLGF--TDTPTVIACNSRLVPRQGDLSLIKAMPQDVIARPDQAQLLIVGSG 238
364  QY      KAAEYKLVNAIGTKYKGRAGGVVKFSAPLAHH-----LTAGADEMLVPSR-----PEPC 412
239  DB      R--YESTLRRLATDVSON-----VKFLGRLEVQDMINTLAAADIFAMPARTRGGLDVEGL 292
413  QY      GLIQLHAMHYGTVVPVVAST--GGLVDVVKEGVTFHMGALNPDKLDDEADADALATVRRAS 471
293  DB      GIYVLEAAQAG-VFVIAGTSGGAPETVTP-ATGLVVEGSDVDKLSSELLIELLDDDPIRRAA 350
472  QY      EVTFAGRYPEMWVANCISODLSWSKPAQKWEGGLE 505
351  DB      MGAAGRAH-----VEAEWSWEIMGERLTNILQ 377

Search completed: June 4, 2003, 15:15:25
Job time : 24.1047 secs

```

```

; LENGTH: 409
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-636-4738

Best Match
Query Local Similarity      6.1%; Score 206; DB 9; Length 409;
                27.2%; Pred. No. 8.5e+07;
Matches 83; Conservative 47; Mismatches 127; Indels 48; Gaps 15;

210 ATPMEDE--KPLTGKTKYKINWL-KGIIAADKLVTSPNVTATEIADAAGVELDTV 266
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
129 AHSLEPDPKREQLGGGVDVSSWSEKNMAYEAVIAVSARKMDSILA-AYPRIEDNV 187
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
267 IRAKGTEGVINGMDIEENPKTKDKFLSAPYDQNSVYAGKAAAKEALQAEGLPVDPTAPL 326
      : | | | | | | | | | | | | | | | | | | | | | | | | | |
188 -----RVVLNGIDTELWQPR-----PTFDD-----AEDSVLRSLG--VDPQRI 224

327 FAFIGLEKQGVDDIILAAPLKILATPKVQIATLGTGKAAYE--KLVNAICTKVKGRAGK 384
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
225 VAFVGRITKQKGVHELIKA--AALFDESVLQVLCAGADPTPEIATAARTALVEELQAKREG 282
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
385 VVKFSAPLA-----HMLTAGADFMVLSRPFECGLIQLHAMHYGTVPVVAAGTGLVDIVK 439
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
283 IFWQDMLGKDKIQIELTA-ADTFVCPSTIYEPLGIVNLEAMAGNTAVVSDVGGIGPWW 341
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
440 EGVGTG--FWHGALNPDKLEADADA--LAATVRRASEVFAGRGYPMWANCISQDLSWS 494
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
342 DGGTGLVHYDENDVETFERDIAEVNKMVADRETAAKFGLAGR--ERATN-----DFSWA 395

495 KPAQK 499
      | |
396 TTAQQ 400

```

RESULT 15
US-09-738-626-5896
; Sequence 5896, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5896
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5896

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 08:28:25 ; Search time 2283.88 Seconds
(without alignments)
16743.883 Million cell updates/sec

Title: US-09-980-771A-6
Perfect score: 1314
Sequence: 1 gcactgacatcgatggt.....ggcgctgtgacacgcgc 1314

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl :

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ro.*
- 12: gb_sy.*
- 13: gb_sy.*
- 14: gb_sy.*
- 15: gb_sy.*
- 16: gb_sy.*
- 17: gb_sy.*
- 18: gb_sy.*
- 19: gb_sy.*
- 20: gb_sy.*
- 21: gb_sy.*
- 22: gb_sy.*
- 23: gb_sy.*
- 24: gb_sy.*
- 25: gb_sy.*
- 26: gb_sy.*
- 27: gb_sy.*
- 28: gb_sy.*
- 29: gb_sy.*
- 30: gb_sy.*
- 31: gb_sy.*
- 32: gb_sy.*
- 33: gb_sy.*
- 34: gb_sy.*
- 35: gb_sy.*
- 36: gb_sy.*
- 37: gb_sy.*
- 38: gb_sy.*
- 39: gb_sy.*
- 40: gb_sy.*
- 41: gb_sy.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1314	100.0	1314	6	AX049327	Sequence
2	1314	100.0	1593	6	AX049329	Sequence
3	1314	100.0	1593	6	AX049325	Sequence
4	1314	100.0	1593	6	AX049323	Sequence
5	1314	100.0	3117	6	AX049322	Sequence
6	1312.4	99.9	3240	8	AF026420	Chlamydom
7	511.8	38.9	5856	8	AF433156	Chlamydom
8	458.4	34.9	2289	8	AF286320	Triticum
9	456.8	34.8	1812	8	AF486514	Hordeum v
10	456.8	34.8	1827	8	AF486515	Hordeum v
11	456.8	34.8	1827	8	AF486518	Hordeum v
12	456.8	34.8	2127	8	AF163319	Triticum
13	456.8	34.8	2311	8	HVWAXYR	Barley mRNA
14	455.2	34.6	1605	8	AF250137	Triticum
15	455.2	34.6	1812	8	AF486519	Hordeum v
16	455.2	34.6	2028	8	AF113844	Triticum
17	453.6	34.5	1827	8	AF486516	Hordeum v
18	453.6	34.5	1827	8	AF486517	Hordeum v
19	432	32.9	2186	8	TAWAXYSS	Wheat waxy
20	432	32.9	2267	8	AY050174	Triticum
21	408.2	31.1	1801	8	AF113843	Triticum
22	407.6	31.0	2115	8	AB089141	Setaria i
23	400.6	30.5	2267	8	AR195560	Sequence
24	390	29.7	1937	8	AB066093	Oryza sat
25	390	29.7	1937	8	AB066094	Oryza sat
26	388.4	29.6	2542	6	AR106491	Sequence
27	388.4	29.6	2542	8	OSWX	O. sativa wa
28	386.4	29.4	2287	8	SHU23945	Sorghum bic
29	310.2	23.6	2168	8	MEGBSS	Sequence
30	306.6	23.3	2270	8	AF210699	M.esculenta
31	298.6	22.7	2221	8	AB029546	Phaseolus
32	285.8	21.8	2211	8	AB071604	Ipomoea b
33	283.8	21.6	3049	8	AF026421	Chlamydom
34	281.8	21.4	2161	6	AX394246	Sequence
35	277.4	21.1	2345	8	AWA6293	Antirrhin
36	276.2	21.0	2124	8	IBU44126	Ipomoea bat
37	271.2	20.6	2092	8	AY094405	Arabidops
38	271.2	20.6	2115	8	AY088544	Arabidops
39	271.2	20.6	2192	8	AY123983	Arabidops
40	265	20.2	2107	8	AF097922	Astragal
41	259.4	19.7	2035	8	PSSTARSIN	P. sativum m
42	236.8	18.0	2081	8	AF109395	Triticum
43	235.2	17.9	1698	8	AF486521	Hordeum v
44	228.4	17.4	2112	8	AY069940	Oryza sat
45	220	16.7	2100	8	PSA345045	Pisum sat

ALIGNMENTS

RESULT 1	AX049327	AX049327	Sequence 6 from Patent WO0071734.	1314 bp	DNA	linear	PAT 12-JAN-2001
LOCUS	AX049327	Sequence 6 from Patent WO0071734.					
DEFINITION	AX049327	Sequence 6 from Patent WO0071734.					
ACCESSION	AX049327	Sequence 6 from Patent WO0071734.					
VERSION	AX049327.1	GI:12226094					
KEYWORDS		synthetic construct.					
SOURCE		synthetic construct.					
ORGANISM		artificial sequences.					
REFERENCE		1 (bases 1 to 1314)					
AUTHORS		D'Hulst,C. and Ball,S.					
TITLE		Starch granules containing a recombinant polypeptide of interest,					
JOURNAL		method for obtaining same and uses					
		Patent: WO 0071734-A 6 30-NOV-2000;					

```

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
1. .1314
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="fragment de l'DNA complet codant la GBSSI de
Chlamydomonas reinhardtii"
<1..>1314
CDS
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC21782.1"
/db_xref="GI:12226095"
/transl_table="ALDIVMVAEAVPWSKTGGLGVDVTLKGLPIELVKRHRVMTIAPR
YDOYADAWTSVVVDIMGEKVFHFKKGVHRVWIDHPFLAKVKGKGLYGRPS
GADYLDNHRFALCKAA TEAARVLPFGPEDCVFVANDMHSALVLLKDEYOPKGO
FYKASVLAHNLAFQGRWEEAFKDKLPQAFDLASDGYAKYVTEATPMEDEK
PLTKQTKYKINWLGIIIAADKLVTSFNPAETIAADAAAGVELDTYIRAKIGIV
NGMDIEENPKDKFLSAPYDONSVTAGKAAKEALOEALPDPVTAFLFAFISGLE
EQGVDTIILAAPLKILATPKVQIATLGKAAAYEKLVNAIGTKYKGRKGVVRFSAPL
AHMLTAGADFMVLPVSRFEPGLIQLHAMHYGTVPVVASTGGLVDIV"
BASE COUNT 238 a 449 c 219 t
ORIGIN
Query Match 100.0%; Score 1314; DB 6; Length 1314;
Best Local Similarity 100.0%; Pred. No. 6.5e-153;
Matches 1314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGTGGACATCGTGATGGTGTGCTGAGTGCGCCCTTGGTCCAAAGCGGGCGCTG 60
Db 1 GCGTGGACATCGTGATGGTGTGCTGAGTGCGCCCTTGGTCCAAAGCGGGCGCTG 60
QY 61 GCGGATGTGACTGGTGGCCCTGCCATTAGTGCTGAAGCGCGGCCACCGCGTCATGACC 120
Db 61 GCGGATGTGACTGGTGGCCCTGCCATTAGTGCTGAAGCGCGGCCACCGCGTCATGACC 120
QY 121 ATTGCCCTCGCTACGACAGTAGCTGACGCTTGGGACACCTCGGTGGTGGTGGACATC 180
Db 121 ATTGCCCTCGCTACGACAGTAGCTGACGCTTGGGACACCTCGGTGGTGGTGGACATC 180
QY 181 ATGGGCGAGAGGTCCCGTACTTCCATCCATCAAGAGGCGTGCACCGCGTGGATT 240
Db 181 ATGGGCGAGAGGTCCCGTACTTCCATCCATCAAGAGGCGTGCACCGCGTGGATT 240
QY 241 GACACCCCTGGTTCCTGGCCAAAGTCTGGGGCAAGACCGGCTCCAAAGCTGTACGGCCC 300
Db 241 GACACCCCTGGTTCCTGGCCAAAGTCTGGGGCAAGACCGGCTCCAAAGCTGTACGGCCC 300
QY 301 CGCTCCGGCGCTGACTACCTGGACACCAAGCGCTTCGCCCTTGTCTGCAAGGCGCT 360
Db 301 CGCTCCGGCGCTGACTACCTGGACACCAAGCGCTTCGCCCTTGTCTGCAAGGCGCT 360
QY 361 ATTGAGCTCGCGCGTGCCTTCCGCGCGGCGGAGGACTGCGTCTTCGTGGCCAAAC 420
Db 361 ATTGAGCTCGCGCGTGCCTTCCGCGCGGCGGAGGACTGCGTCTTCGTGGCCAAAC 420
QY 421 GACTGGCACTCCGCGCTGGTGGCCGCTGCTGTGAAGACAGTAGTACCAGCCCAAGGGCCAG 480
Db 421 GACTGGCACTCCGCGCTGGTGGCCGCTGCTGTGAAGACAGTAGTACCAGCCCAAGGGCCAG 480
QY 481 TTCACCAAGCCAGTCCGCTGGCTGCTATCCACACATCCCTTCAGGGCCGCTATGG 540
Db 481 TTCACCAAGCCAGTCCGCTGGCTGCTATCCACACATCCCTTCAGGGCCGCTATGG 540
QY 541 GAGGAGGCTTCAAGGACAGAGTCCGCCCGAGCGCCCTTGTGACAGCTGGCCCTTCG 600
Db 541 GAGGAGGCTTCAAGGACAGAGTCCGCCCGAGCGCCCTTGTGACAGCTGGCCCTTCG 600
QY 601 GACGGCTATGCCAAGGTTTACACTGAGGCCACCCCGATGAGGAGGACGAGAACCCCGG 660
Db 601 GACGGCTATGCCAAGGTTTACACTGAGGCCACCCCGATGAGGAGGACGAGAACCCCGG 660
QY 661 CTGACGGGAAGACCTACAGAAGATCACTGGCTGAAGGCTGACATTCATCGCCGCGGAC 720
```

```

Db 661 CTGACGGGAAGACCTACAGAAGATCACTGGCT3AAGGTTGCAATATCGCCGCGAC 720
QY 721 AAGCTGTGACTGTGTCGCCCAACTACGCGACCGAGATCGCTGCGATGCGCGCGCGGT 780
Db 721 AAGCTGTGACTGTGTCGCCCAACTACGCGACCGAGATCGCTGCGATGCGCGCGCGGT 780
QY 781 GTGAGCTGGACACCGCTATCCGCGCAAGGGCATTTGAGGGCATTTGTAACGGCATGAC 840
Db 781 GTGAGCTGGACACCGCTATCCGCGCAAGGGCATTTGAGGGCATTTGTAACGGCATGAC 840
QY 841 ATTGAGAGTGGAAACCCCAAGACCGCAAGTTCCTGCTGCTGGGCCCTAGCACCAGAACGC 900
Db 841 ATTGAGAGTGGAAACCCCAAGACCGCAAGTTCCTGCTGCTGGGCCCTAGCACCAGAACGC 900
QY 901 GTCTACCGCGCAAGCGCGCCCAAGGAGGCGCTGACGCGCGAGCTGGGCTGCTGCTGTG 960
Db 901 GTCTACCGCGCAAGCGCGCCCAAGGAGGCGCTGACGCGCGAGCTGGGCTGCTGCTGTG 960
QY 961 GACCCACCGCCCGCCCTTGTGCGCTTCATCGCGCGCTGAGAGGAGAGAGGGTGTGGAC 1020
Db 961 GACCCACCGCCCGCCCTTGTGCGCTTCATCGCGCGCTGAGAGGAGAGAGGGTGTGGAC 1020
QY 1021 ATCATCTGGCGCGCTGCCCAAGATCTGCGCACCCCGCCAGGTGCAGATGCCATCGT 1080
Db 1021 ATCATCTGGCGCGCTGCCCAAGATCTGCGCACCCCGCCAGGTGCAGATGCCATCGT 1080
QY 1081 GGTACCGCGCAAGCGCGCTACGAGAAGTGTGAACGCGCATCGCGCACCAAGTACAAGGC 1140
Db 1081 GGTACCGCGCAAGCGCGCTACGAGAAGTGTGAACGCGCATCGCGCACCAAGTACAAGGC 1140
QY 1141 CGCGCCAAAGCGGTGTCAAGTTCGCGCGCCCTGGGCGACATGCTCACCGCGCGGCC 1200
Db 1141 CGCGCCAAAGCGGTGTCAAGTTCGCGCGCCCTGGGCGACATGCTCACCGCGCGGCC 1200
QY 1201 GACTTCATGTGTGTCCTCGCTGCTGAGCGCTGCGCGCTGATCCAGCTGCACGCGCATG 1260
Db 1201 GACTTCATGTGTGTCCTCGCTGCTGAGCGCTGCGCGCTGATCCAGCTGCACGCGCATG 1260
QY 1261 CACTACGCTACCGTCCCGCTGTAGCTCCACCGCGCGCTGGTGCAGACCGCTC 1314
Db 1261 CACTACGCTACCGTCCCGCTGTAGCTCCACCGCGCGCTGGTGCAGACCGCTC 1314

RESULT 2
AX049329 LOCUS AX049329 1593 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 8 from Patent WO0071734.
ACCESSION AX049329
VERSION AX049329.1 GI:12226096
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 1593).
AUTHORS D'Hulst,C. and Ball,S.
TITLE Starch granules containing a recombinant polypeptide of interest,
METHOD for obtaining same and uses
PATENT: WO 0071734-A 8 30-NOV-2000;
JOURNAL CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source
1. .1593
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="fragment de l'DNA complet codant la GBSSI de
Chlamydomonas reinhardtii"
<1..>1593
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC21783.1"
/db_xref="GI:12226097"
/translation="ALDIVMVAEAVPWSKTGGLGVDVTLKGLPIELVKRHRVMTIAPR
```


YDOYADADTSVVVDITMGKVKVRFHSIKGVHVHWITDHPWFLAKVWGKTSKUYLGPBS
GADYLDNHNKFAFLCKAETAARVLFKFGCEDCVFANDWMSALVPLVLLIKDEYQPGQ
FTKAKSVLAHNIAFTQORWEEAFKFTQPAQFDKLAFTSDGAKYKVTIATPEEDEK
PLPTGTRKKNLWKGITIAADKLVSPNYATETAAADAGGVELDVTIRAKGIEGIV
NMGIIEBNPKTDLSAPYDQNSVYAGKAARKEALQAEGLPDTAFIFAGIGLE
EOKHVDIIAALPKILATPKVQITILGTGKAAYEKLVNATIKYKGVKVFKSAPL
AEMDITAGDFMLVSPFEPGQITLHAMHYGTVPVASTGGLVDTKRGVGTGPHMGAJ
NPDKLEADADALAAATVRASEVFAAGRYPEMVANCISDLSWSKPAQKWEGGLEEVV
YKGKGVATAKKEIKVPVAKPIR"

290 a 539 c 510 g 254 t

BASE COUNT
ORIGIN

Query Match	100.0%;	Score 1314;	DB 6;	Length 1593;
Best Local Similarity	100.0%;	Pred. No. 6.2e-153;		
Matches 1314;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GCCTGGACATCGTGATGGTTGCTGCTGAGGTGCGCCCTTGGTCCCAAGACGGCGGCGCTG	60	
Db	1			
QY	61	GGCGATGTGACTGGTGCCCTGCCCTATTGAGTGGTCAAGCGCGGCCCAACCGCGTCATGACC	120	
Db	61	GGCGATGTGACTGGTGCCCTGCCCTATTGAGTGGTCAAGCGCGGCCCAACCGCGTCATGACC	120	
QY	121	ATTGCCCCCTCGCTACGACCAAGTACGCTGACCCATCAAGAAAGGGCGTGACCCCGTGTGGATT	240	
Db	121	ATTGCCCCCTCGCTACGACCAAGTACGCTGACCCATCAAGAAAGGGCGTGACCCCGTGTGGATT	240	
QY	181	ATGGCGGAGAAGTCCGCTACTTCCACTCCATCAAGAAAGGGCGTGACCCCGTGTGGATT	300	
Db	181	ATGGCGGAGAAGTCCGCTACTTCCACTCCATCAAGAAAGGGCGTGACCCCGTGTGGATT	300	
QY	241	GACCACCCCTGGTTCTCTGGSCCAAGTGCTGGGGCAAGACCGCGCTCCAAAGCTGACGGCCCC	360	
Db	241	GACCACCCCTGGTTCTCTGGSCCAAGTGCTGGGGCAAGACCGCGCTCCAAAGCTGACGGCCCC	360	
QY	301	CGCTCCGGCGCTGACTACCTGGACACCAACGAGCGTTGCGCCCTGTTCTCAAGGCGCGT	420	
Db	301	CGCTCCGGCGCTGACTACCTGGACACCAACGAGCGTTGCGCCCTGTTCTCAAGGCGCGT	420	
QY	361	ATTGAGGCTCCCGCGTGTGCTGCGCTTCGGCCCGCGGAGGACTGCGTCTTCGTGGCCAAAC	480	
Db	361	ATTGAGGCTCCCGCGTGTGCTGCGCTTCGGCCCGCGGAGGACTGCGTCTTCGTGGCCAAAC	480	
QY	421	GATGGGACTCCGCGCTGGTGCCGCTCTCTGCTGAAAGGACGAGTACCAGCCCAAGAGGCCAG	540	
Db	421	GATGGGACTCCGCGCTGGTGCCGCTCTCTGCTGAAAGGACGAGTACCAGCCCAAGAGGCCAG	540	
QY	481	TTCCACCAAGGCCAAGTCCGCTGCTGCTATCCACAAATGCGCTTCCAGGCGCGCATGTGG	600	
Db	481	TTCCACCAAGGCCAAGTCCGCTGCTGCTATCCACAAATGCGCTTCCAGGCGCGCATGTGG	600	
QY	541	GAGGAGCGCTTTCGAAGGACACGAAGTGCCTCCAGCGCGCTTTCACAAAGCTGGCGCTTCTCG	660	
Db	541	GAGGAGCGCTTTCGAAGGACACGAAGTGCCTCCAGCGCGCTTTCACAAAGCTGGCGCTTCTCG	660	
QY	601	GACGGGTATGCCAAGGTTTACATGAGGCGCACCCCATGAGGAGGACGAGAAAGCCCGCG	720	
Db	601	GACGGGTATGCCAAGGTTTACATGAGGCGCACCCCATGAGGAGGACGAGAAAGCCCGCG	720	
QY	661	CTACCGGAAAGACCTTACAAAGAGATCACTGCGCTGAAGGGTGGCATTTATCGCGCGGAC	780	
Db	661	CTACCGGAAAGACCTTACAAAGAGATCACTGCGCTGAAGGGTGGCATTTATCGCGCGGAC	780	
QY	721	AAGCTGTGACTGTGCGCCCACTACGCGACCGAGATCGTGCCCATGCGCCCGCGCGGT	840	
Db	721	AAGCTGTGACTGTGCGCCCACTACGCGACCGAGATCGTGCCCATGCGCCCGCGCGGT	840	
QY	781	GTGGAGCTGGACACCGTTCATCCGCGCAAGGCGATTGAGGGCATTTGTAACGCCATGGAC	900	
Db	781	GTGGAGCTGGACACCGTTCATCCGCGCAAGGCGATTGAGGGCATTTGTAACGCCATGGAC	900	
QY	841	ATTGAGGAGTGGAAACCCCAAGACCGCAAGTTCTCTGTGCGCGCTTACGACCAAGACACG	960	

Db	841	ATTGAGGAGTGGAAACCCCAAGACCCACAAAGTTCCTGTGCGCCCTACGACCAAGACAGC	900
Qy	901	GTCTACGCCGCGCAAGCGCGCCCAAGAGAGCCCTGCAGAGCGGAGCTGGGCGCTGCCTGTG	960
Db	901	GTCTACGCCGCGCAAGCGCGCCCAAGAGAGCCCTGCAGAGCGGAGCTGGGCGCTGCCTGTG	960
Qy	961	GACCCACCGCCCGCCCTGTTCGCCCTTCATCGCGCGCCTGGAGGACGACAAAGGTGTGGAC	1020
Db	961	GACCCACCGCCCGCCCTGTTCGCCCTTCATCGCGCGCCTGGAGGACGACAAAGGTGTGGAC	1020
Qy	1021	ATCATCTGGCGGCCCTGCCCAAGATCTGCCACCCCAAGGTGCAGATCGCCATCCTG	1080
Db	1021	ATCATCTGGCGGCCCTGCCCAAGATCTGCCACCCCAAGGTGCAGATCGCCATCCTG	1080
Qy	1081	GGTACCGGCAAGCGCGCCTACGAGAACTGTGAAGCCATCGGCACCAAGTACAAGGCG	1140
Db	1081	GGTACCGGCAAGCGCGCCTACGAGAACTGTGAAGCCATCGGCACCAAGTACAAGGCG	1140
Qy	1141	CGCGCCAAAGCGGTGTCAAGTTCTCGGCGCCCTGGCGCACATGCTCACGCGCGGCGCC	1200
Db	1141	CGCGCCAAAGCGGTGTCAAGTTCTCGGCGCCCTGGCGCACATGCTCACGCGCGGCGCC	1200
Qy	1201	GACTTCATGCTGTGGTGGCCTCGCGGTTGAGCCCTGCGGCGCTGATCCAGCTGCAGCGCCATG	1260
Db	1201	GACTTCATGCTGTGGTGGCCTCGCGGTTGAGCCCTGCGGCGCTGATCCAGCTGCAGCGCCATG	1260
Qy	1261	CACTACGGTACCGTGGCGGTGGTAGCTCCACCGCGGCGCTGGTGACACCGTC	1314
Db	1261	CACTACGGTACCGTGGCGGTGGTAGCTCCACCGCGGCGCTGGTGACACCGTC	1314

[illegible]

```

mature
<i>. >1953
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/db_xref="GI:12226093"
/protein_id="CAC21781.1"
/transl="ALD1VMAAEVAPWSKTCGLDVTGLPIELVKRGHYMTIAPR
YDQYADAWDFSVVVD1MGEXRVYFHSIKGVHVVTDHPWLAKVYGLKSPGRS
GADYLDNHKEPALCKAA1BAARVLFGPCEDCVFVNDPHSLVPLVLLKLSYKPGQ
FTAKSVLA1THNTAFQGRWEAEAFKOTKLPQAAFDKLA1SDGYAKVY1EAT1PWEDEK
PPLTGKTYK1NLNKG1IAADKLNV1SNYATE1PAADAAGVGLDVT1VRAGFA1EG1V
NGMD1EWN1K1DKF1L5AP1DQNSV1YAGKAAKEALQAE1GLP1DVT1IRAF1IG1E
EQGVD1LAAL1PK1IAT1KVQ1I1LH1TGKAAV1EKLVA1IGTKYGRAGVYKFSAPL
AHMT1AGAD1ML1PFS1REF1PCGL1Q1LHMG1YV1VVA1STGLV1D1KEV1TG1FHMG1AL
NP0K1GD2ADALAA1TVR1RA1SEV1FAGG1R1PEM1VANG1ISQD1L5SK1PAQK1G1LEEV
YUGK1GVATA1KEIK1EY1VAEK1IPGDL1P1Y1SAP1NTLK1VSAS1VEGNG1AAAP1KVGT1AP
AMGAW1RA1IT1PSG1PAAAT1PV1TYK1PAL1PATA1PK1TAG1KLAGE1AST1T1SENG1AA1S
NNGNG1SAS1K1T5AAK1PLV1SAAT1PKK1SA"

```


Db 172 GCGTGGACATCGTGATGGTGTGCTGAGGTGCGCCCTTGGTCCAAAGCGGCGGCTG 231
QY 61 GGCATGTGACTGTGGCTTGCCTATTAGTGTGTCTAAGCGCGGCCACCGGTATGAGCC 120
Db 232 GCGCATGTGACTGTGGCTTGCCTATTAGTGTGTCTAAGCGCGGCCACCGGTATGAGCC 291
QY 121 ATTGCCCTCGCTACGACCACTGAGTGTGACGCTTGGGCGGACACTCGTGTGGTGTGATC 180
Db 292 ATTGCCCTCGCTACGACCACTGAGTGTGACGCTTGGGCGGACACTCGTGTGGTGTGATC 351
QY 181 ATGGCGGAGAGGTCGCTACTTCCACTTCCATCAAGAGGCGGTGACCGGCTGTGGATT 240
Db 352 ATGGCGGAGAGGTCGCTACTTCCACTTCCATCAAGAGGCGGTGACCGGCTGTGGATT 411
QY 241 GACACCCCTGGTTCCTTGGCGCAAGTCTTGGGCGAAGACCGGCTCCAGCTGTACGGCCCC 300
Db 412 GACACCCCTGGTTCCTTGGCGCAAGTCTTGGGCGAAGACCGGCTCCAGCTGTACGGCCCC 471
QY 301 CGCTCCGGCGCTGACTACTTGGCAACCAAGCGCTTGGCGGCTTGTCTGCAAGGCGGCT 360
Db 472 CGCTCCGGCGCTGACTACTTGGCAACCAAGCGCTTGGCGGCTTGTCTGCAAGGCGGCT 531
QY 361 ATTAGAGCTGCCCGCTGTGCTGCTTCCGCGCGGCGGAGGACTGCGTCTTGGTGGCCAA 420
Db 532 ATTAGAGCTGCCCGCTGTGCTGCTTCCGCGCGGCGGAGGACTGCGTCTTGGTGGCCAA 591
QY 421 GACTGGCACTCCCGCTGGTGGCGGCTTGGCGGCGGCGGAGGACTGCGTCTTGGTGGCCAA 480
Db 592 GACTGGCACTCCCGCTGGTGGCGGCTTGGCGGCGGCGGAGGACTGCGTCTTGGTGGCCAA 651
QY 481 TTCACCAAGGCCAAGTGGTGGCTTATCCACAACATCGCTTCCAGGCGGCGATGCG 540
Db 652 TTCACCAAGGCCAAGTGGTGGCTTATCCACAACATCGCTTCCAGGCGGCGATGCG 711
QY 541 GAGAGGCTTTCAGGACACGAGCTGCCCGCGGCGGCGGCTTTCAGAGCTGGCGTTCG 600
Db 712 GAGAGGCTTTCAGGACACGAGCTGCCCGCGGCGGCGGCTTTCAGAGCTGGCGTTCG 771
QY 601 GAGGCTATCCAGGTTTACACTGAGCTGAGGCGGCGGCGGCTTTCAGAGCTGGCGTTCG 660
Db 772 GAGGCTATCCAGGTTTACACTGAGGCGGCGGCGGCGGCTTTCAGAGCTGGCGTTCG 831
QY 661 CTGACGGGAAGACCTTACAGAGATCACTGGCTGAAGGCTGAGTATTCGCGCGGCGG 720
Db 832 CTGACGGGAAGACCTTACAGAGATCACTGGCTGAAGGCTGAGTATTCGCGCGGCGG 891
QY 721 AAGCTGGTACTGTGCGGCCAACTACGGGACCGAGATCGCTGCGGATGCGCGGCGG 780
Db 892 AAGCTGGTACTGTGCGGCCAACTACGGGACCGAGATCGCTGCGGATGCGCGGCGG 951
QY 781 GTGGAGCTGGACACCGCTATCCGCGCAAGGGGCAATTGAGGGCAATTGAGGCAATG 840
Db 952 GTGGAGCTGGACACCGCTATCCGCGCAAGGGGCAATTGAGGGCAATTGAGGCAATG 1011
QY 841 ATTGAGAGTGAACCCCAAGACCGCAAGTTCCTGTCTGCGGCTTACGACCAAGACAG 900
Db 1012 ATTGAGAGTGAACCCCAAGACCGCAAGTTCCTGTCTGCGGCTTACGACCAAGACAG 1071
QY 901 GTCTAGCGCGGCAAGCGCGGCCAAGGAGGCGCTTCAGGCGGAGCTGGGCTTGCCTGTG 960
Db 1072 GTCTAGCGCGGCAAGCGCGGCCAAGGAGGCGCTTCAGGCGGAGCTGGGCTTGCCTGTG 1131
QY 961 GACCCACGCGGCGGCTTTCGCGCTTATCGGCGGCGCTTGAGGAGCAAGAGGTGTGGAC 1020
Db 1132 GACCCACGCGGCGGCTTTCGCGCTTATCGGCGGCGCTTGAGGAGCAAGAGGTGTGGAC 1191
QY 1021 ATCATCTGCGCGGCTTGCCTGAGAGTTCCTGGCCACCCCAAGTGCAGATCGCATCTTG 1080
Db 1192 ATCATCTGCGCGGCTTGCCTGAGAGTTCCTGGCCACCCCAAGTGCAGATCGCATCTTG 1251
QY 1081 GGTACCGGCAAGCGCGGCTTACGAGAGCTGGTGAAGCGGCTTGCAGGCGGCTTGCAGG 1140
Db 1252 GGTACCGGCAAGCGCGGCTTACGAGAGCTGGTGAAGCGGCTTGCAGGCGGCTTGCAGG 1311

QY 1141 CGGCCAAAGCGGTGGTCAAGTCTTCGGCGGCCCTTGGCGCACATGCTACCGCGCGGCGC 1200
Db 1312 CGGCCAAAGCGGTGGTCAAGTCTTCGGCGGCCCTTGGCGCACATGCTACCGCGCGGCGC 1371
QY 1201 GACTTCATGCTGGTGGCCCTCGCGCTTCGAGCCCTCGGCGCTGATCCAGTGCACGCCATG 1260
Db 1372 GACTTCATGCTGGTGGCCCTCGCGCTTCGAGCCCTCGGCGCTGATCCAGTGCACGCCATG 1431
QY 1261 CACTACGCTACCGTCCCGTGTAGCTTCCACCGCGGCGCTGGTGCACACGCTC 1314
Db 1432 CACTACGCTACCGTCCCGTGTAGCTTCCACCGCGGCGCTGGTGCACACGCTC 1485

RESULT 5
AX049322
LOCUS AX049322 3117 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 1 from Patent WO0071734.
ACCESSION AX049322
VERSION AX049322.1 GI:12226089
KEYWORDS
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE 1 (bases 1 to 3117)
AUTHORS D'Hulst,C. and Ball,S.
TITLE Starch granules containing a recombinant polypeptide of interest,
method for obtaining same and uses
Patent: WO 0071734-A 1 30-NOV-2000;
JOURNAL PATENT NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
Location/Qualifiers
1..3117
/organism="Chlamydomonas reinhardtii"
/db_xref="taxon:3055"
BASE COUNT 599 a 994 c 1011 g 513 t
ORIGIN

Query Match 100.0%; Score 1314; DB 6; Length 3117;
Best Local Similarity 100.0%; Pred. No. 5.3e-153;
Matches 1314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTGGACATCGTGATGGTGTGCTGAGGTGCGCCCTTGGTCCAAAGCGGCGGCTG 60
Db 186 GCGTGGACATCGTGATGGTGTGCTGAGGTGCGCCCTTGGTCCAAAGCGGCGGCTG 245
QY 61 GCGCATGTGACTGTGGCTTGCCTATTAGTGTGTCTAAGCGCGGCCACCGGTATGAGCC 120
Db 246 GCGCATGTGACTGTGGCTTGCCTATTAGTGTGTCTAAGCGCGGCCACCGGTATGAGCC 305
QY 121 ATTGCCCTCGCTACGACCACTGAGTGTGACGCTTGGCGCTGGGACACTCGGTGGTGTGACATC 180
Db 306 ATTGCCCTCGCTACGACCACTGAGTGTGACGCTTGGCGCTGGGACACTCGGTGGTGTGACATC 365
QY 181 ATGGCGGAGAGTGTGCTTCCACTTCCATCAAGAGGCGGTGACCGGCTGTGGATT 240
Db 366 ATGGCGGAGAGTGTGCTTCCACTTCCATCAAGAGGCGGTGACCGGCTGTGGATT 425
QY 241 GACACCCCTGGTTCCTGGCGCAAGTCTGGGCGAAGACCGGCTCCAGCTGTACGGCCCC 300
Db 426 GACACCCCTGGTTCCTGGCGCAAGTCTGGGCGAAGACCGGCTCCAGCTGTACGGCCCC 485
QY 301 CGTCCGGCGCTGACTTACCTTGGCAACCAAGCGCTTTCGCGCTTGTCTGCAAGGCGGCT 360
Db 486 CGTCCGGCGCTGACTTACCTTGGCAACCAAGCGCTTTCGCGCTTGTCTGCAAGGCGGCT 545
QY 361 ATTAGAGCTGCCCGGCTGTGCTTGGCGGCGGCGGAGGACTGCGTCTTGGTGGCCAA 420
Db 546 ATTAGAGCTGCCCGGCTGTGCTTGGCGGCGGCGGAGGACTGCGTCTTGGTGGCCAA 605.
QY 421 GACTGGCACTCCCGCTTGGTGGCGGCTTGCCTGCTGAAGGACGAGTACGAGCCAGGCGG 480
Db 606 GACTGGCACTCCCGCTTGGTGGCGGCTTGCCTGCTGAAGGACGAGTACGAGCCAGGCGG 665.

```

QY 481 TTCACCAAGGCCAAGTCGGTGGTATCCCAACATCGCCTTCAGGCGCCGATGTGG 540
|
|
|
Db 666 TTCACCAAGGCCAAGTCGGTGGTATCCCAACATCGCCTTCAGGCGCCGATGTGG 725
|
|
|
QY 541 GAGGAGGCTTTCAAGGACACGAAGCTGCCCCAGGCGCCCTTTGACAAGCTGGCCTTCTCG 600
|
|
|
Db 726 GAGGAGGCTTTCAAGGACACGAAGCTGCCCCAGGCGCCCTTTGACAAGCTGGCCTTCTCG 785
|
|
|
QY 601 GAGGCTATGCCAAGCTTTACACTGAGGCGCCACCCCATGAGGAGGACGAGAGCCGCCG 660
|
|
|
Db 786 GAGGCTATGCCAAGCTTTACACTGAGGCGCCACCCCATGAGGAGGACGAGAGCCGCCG 845
|
|
|
QY 661 CTGACGGGAAGACCTACAAGAGATCACTGCTGAAGGCTGGCCTATTATCGCCGCGAC 720
|
|
|
Db 846 CTGACGGGAAGACCTACAAGAGATCACTGCTGAAGGCTGGCCTATTATCGCCGCGAC 905
|
|
|
QY 721 AAGCTGGTGACTGTGCGCCCACTAGCGGACCGAGATGCTGCGATGCCGCGCGGCT 780
|
|
|
Db 906 AAGCTGGTGACTGTGCGCCCACTAGCGGACCGAGATGCTGCGATGCCGCGCGGCT 965
|
|
|
QY 781 GTGAGCTGACACCGCTATCCGCGCAAGGCGATTGAGGCGATTGTGAACGGCGATGGAC 840
|
|
|
Db 966 GTGAGCTGACACCGCTATCCGCGCAAGGCGATTGAGGCGATTGTGAACGGCGATGGAC 1025
|
|
|
QY 841 ATTGAGGAGTGAACCCCAAGACCGCAAGTTCTCTGCTGCGCCCTACGACCAAGACAGC 900
|
|
|
Db 1026 ATTGAGGAGTGAACCCCAAGACCGCAAGTTCTCTGCTGCGCCCTACGACCAAGACAGC 1085
|
|
|
QY 901 GTCTAGCGCGGCAAGCGCGCGCAAGGAGGCGCTCGAGCGCGAGCTGGCCCTGCCCTGTG 960
|
|
|
Db 1086 GTCTAGCGCGGCAAGCGCGCGCAAGGAGGCGCTCGAGCGCGAGCTGGCCCTGCCCTGTG 1145
|
|
|
QY 961 GACCCACACCGCCCGCTGTTGCGCTTCATCGCGCGCTGAGGAGGAGAGGCTGTGCAC 1020
|
|
|
Db 1146 GACCCACACCGCCCGCTGTTGCGCTTCATCGCGCGCTGAGGAGGAGAGGCTGTGCAC 1205
|
|
|
QY 1021 ATCATCTGCGCGCCCTGCCCCAAGATCCTGGCCACCCCCAAGGTGCAGATCGCCATCCTG 1080
|
|
|
Db 1206 ATCATCTGCGCGCCCTGCCCCAAGATCCTGGCCACCCCCAAGGTGCAGATCGCCATCCTG 1265
|
|
|
QY 1081 GGTACCGGCAAGCGCGCTACGAGAGCTGGTGAACGCCATCGGCACCAAGTCAAGGCG 1140
|
|
|
Db 1266 GGTACCGGCAAGCGCGCTACGAGAGCTGGTGAACGCCATCGGCACCAAGTCAAGGCG 1325
|
|
|
QY 1141 CGCGCCCAAGGCGGTGTCAAGTTCTCGCGCGCCCTGCGCGCACATGCTCACCGCGCGCC 1200
|
|
|
Db 1326 CGCGCCCAAGGCGGTGTCAAGTTCTCGCGCGCCCTGCGCGCACATGCTCACCGCGCGCC 1385
|
|
|
QY 1201 GACTTCATGCTGTGCGCCTCGCGCTTCGAGCCCTGCGCGCTGATCCAGCTGCAGCGCCATG 1260
|
|
|
Db 1386 GACTTCATGCTGTGCGCCTCGCGCTTCGAGCCCTGCGCGCTGATCCAGCTGCAGCGCCATG 1445
|
|
|
QY 1261 CACTACGCTACGCTGCGCGGTGAGCTTCACCGCGCGCCCTGCTGCGACACCGTC 1314
|
|
|
Db 1446 CACTACGCTACGCTGCGCGGTGAGCTTCACCGCGCGCCCTGCTGCGACACCGTC 1499
|
|
|
RESULT 6
AF026420 3240 bp mRNA linear PLN 05-NOV-2001
LOCUS Chlamydomonas reinhardtii granule-bound starch synthase I precursor
DEFINITION (STA2) mRNA, complete cds.
ACCESSION AF026420
VERSION AF026420.3 GI:16716334
KEYWORDS Chlamydomonas reinhardtii.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE D'Hulst,C., Wattedled,F., Ral,J.-P., Abel,G.J., Kossmann,J. and
AUTHORS Ball,S.G.

```

```

TITLE Cloning of a cDNA encoding for the GBSSI in the green alga
Chlamydomonas reinhardtii
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3240)
AUTHORS D'Hulst,C., Abel,G.J., Kossmann,J. and Ball,S.G.
TITLE Direct Submission
JOURNAL Submitted (23-SEP-1997) Genetique Microbienne, Lab. Chimie
Biologique UMR111 CNRS, Univ. Sci. Tech. de Lille, Villeneuve
d'Ascq Cedex 59655, France
REFERENCE 3 (bases 1 to 3240)
AUTHORS D'Hulst,C., Wattedled,F., Ral,J.-P., Abel,G.J., Kossmann,J. and
Ball,S.G.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2000) Groupe de Glycobiologie des Protistes,
Laboratoire de Chimie Biologique, UMR 8576 du CNRS, Universite des
Sciences et Technologies de Lille, Villeneuve d'Ascq Cedex 59655,
France
REMARK Sequence update by submitter
REFERENCE 4 (bases 1 to 3240)
AUTHORS D'Hulst,C., Wattedled,F., Ral,J.-P., Abel,G.J., Kossmann,J. and
Ball,S.G.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) Groupe de Glycobiologie des Protistes,
Laboratoire de Chimie Biologique, UMR 8576 du CNRS, Universite des
Sciences et Technologies de Lille, Villeneuve d'Ascq Cedex 59655,
France
REMARK Sequence update by submitter
COMMENT On Nov 5, 2001 this sequence version replaced gi:8573759.
FEATURES
source
1..3240
/organism="Chlamydomonas reinhardtii"
/strain="J137C"
/db_xref="taxon:3055"
/clone="CD142"
1..3240
/gene="STA2"
138..2264
/gene="STA2"
/EC_number="2.4.1.21"
/function="ADP-Glucose:alpha-1,
4-D-glucan-4-alpha-D-glucosyltransferase"
/notes="GBSSI"
/codon_start=1
/product="granule-bound starch synthase I precursor"
/protein_id="AACI1969.3"
/db_xref="GI:16716335"
/translat="MAVASTSPSSARPIVINAASFGVKKKTANOLLRELARGSARKST
SRSAVTGATCATCALDIVMAAEVAPMSKTGGLGVDTPGLPIELVKGHRVMTIAPRY
DOYADAWDTSVVDIMGEKIVYFHSIKGVHRVIDHPWFLAKVWGKSLYGPGRSG
ADYLDNHKREALEFCKALEARVLPEFGPGEDCVFANDWSALVPVLLKDEYOPKQGF
TKAKSVLAHINIAFOGRMWEAEKDKLPQAAFDKLAFSQGYAKYVTEATPMEDKXP
PLTGKTYKKINWLKGLIAADKLIVTSPNATEADAAGGVELDTPVIRAKGLEGIYN
GMDIEWNPKTDKFLSVYPDONSIVAGKAAKALQAEGLPVDPTAPFATFGRLEE
HMLTAGDEMLVPSRPFCGLIOLHAMHYGTVPVASTGGLVDTKRGAKGVYKFSAPLA
PKLDEADADALAATVPRASEVFAGGYPEMVANCI SODLSWSKPAOKWGLLEEVY
GKGVATAKKEEIKVPVAEKIPGLPVAISAPNTLKFVSASVEGNGAAAPKVGTTAPA
MGAWRATTPSGPSAPAAATPKVTYKLPALPATAKPTAGLKLAGEASTTSTSENGAASN
GNGNGASAKTSAAKPLVSAATRAKS"
transit_peptide 138..308
/gene="STA2"
mat_peptide 309..2261
/gene="STA2"
/product="granule-bound starch synthase I"
BASE COUNT 625 a 1038 c 1044 g 533 t
ORIGIN
Query Match 99.9%; Score 1312.4; DB 8; Length 3240;
Best local similarity 99.9%; Pred. No. 8.2e-153;
Matches 1313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGCGCTGGACATCGCATGCTGCTGCTGAGGTGCGCCCTTGCTCCAGACGGCGCGCTG 60
|
|
|

```

Db 309 GCGCTGACATCGTGATGGTGTGCTGAGGTGCGCCCTTGCTCCACGACGGCGGCTG 368
QY 61 GGCATGTGACTGTGGCCCTGCCTATTAGTGTGTCAAGCGCGCCACCGCGTTCATGACC 120
Db 369 GCGCATGTGACTGTGGCCCTGCCTATTAGTGTGTCAAGCGCGCCACCGCGTTCATGACC 428
QY 121 ATTGCCCTCGCTACGACCACTAGCTGACGCTTGGACACCTCGGTGGTGTGGATC 180
Db 429 ATTGCCCTCGCTACGACCACTAGCTGACGCTTGGACACCTCGGTGGTGTGGATC 488
QY 181 ATGGCGGAGAGTTCGCTACTTCCACTCCATCAAGAGGCGTGCACCGGTGTGGATT 240
Db 489 ATGGCGGAGAGTTCGCTACTTCCACTCCATCAAGAGGCGTGCACCGGTGTGGATT 548
QY 241 GACACCCCTGGTTCCTGGCCAGGCTGTGGGCAAGACCGGCTCCAAAGCTGTACGGCCCC 300
Db 549 GACACCCCTGGTTCCTGGCCAGGCTGTGGGCAAGACCGGCTCCAAAGCTGTACGGCCCC 608
QY 301 CGCTCCGGCGCTGACTACTTGGACAACCAAGGCTTCGCCCTGTTCGCAAGCGCGCT 360
Db 609 CGCTCCGGCGCTGACTACTTGGACAACCAAGGCTTCGCCCTGTTCGCAAGCGCGCT 668
QY 361 ATTGAGCTCCCGCGTGTGCTTGGCCCGGCGGAGGACTCGCTTCGTGGCCAAAC 420
Db 669 ATTGAGCTCCCGCGTGTGCTTGGCCCGGCGGAGGACTCGCTTCGTGGCCAAAC 728
QY 421 GACTGGCACTCCCGCTGGTGGCCCTTGGCCCGGCGGAGGACTCGCTTCGTGGCCAAAC 480
Db 729 GACTGGCACTCCCGCTGGTGGCCCTTGGCCCGGCGGAGGACTCGCTTCGTGGCCAAAC 788
QY 481 TTCACCAAGGCCAAGTCGGTGTGCTATCCACAACATCCCTTCCAGGCGCCGATG 540
Db 789 TTCACCAAGGCCAAGTCGGTGTGCTATCCACAACATCCCTTCCAGGCGCCGATG 848
QY 541 GAGGAGCTTCAAGGACAGAGTGCCTTGGCCCGGCGGAGGACTCGCTTCGTGGCCAAAC 600
Db 849 GAGGAGCTTCAAGGACAGAGTGCCTTGGCCCGGCGGAGGACTCGCTTCGTGGCCAAAC 908
QY 601 GAGGCTATGCCAAGCTTACACTGAGGCGACCCCGCTATGAGGAGGACGAGAGCCCGG 660
Db 909 GAGGCTATGCCAAGCTTACACTGAGGCGACCCCGCTATGAGGAGGACGAGAGCCCGG 968
QY 661 CTGACGGGAAAGACCTTACAGAGATCAACTGGCTGAAGGTTGGCTATTCGCGCGGAC 720
Db 969 CTGACGGGAAAGACCTTACAGAGATCAACTGGCTGAAGGTTGGCTATTCGCGCGGAC 1028
QY 721 AAGCTGTGACTGTGCGCCCACTACGCGACCGAGATCGCTCCGATGCGCGCGCGGT 780
Db 1029 AAGCTGTGACTGTGCGCCCACTACGCGACCGAGATCGCTCCGATGCGCGCGCGGT 1088
QY 781 GTGGAGCTGGACACCGCTATCCGCGCAAGGCAATGAGGCAATGTAACGCGATGGAC 840
Db 1089 GTGGAGCTGGACACCGCTATCCGCGCAAGGCAATGAGGCAATGTAACGCGATGGAC 1148
QY 841 ATTGAGGAGTGAACCCCAAGACCGACAAAGTTCCTGTCTGCGCCCTTACGACCAAGACAGC 900
Db 1149 ATTGAGGAGTGAACCCCAAGACCGACAAAGTTCCTGTCTGCGCCCTTACGACCAAGACAGC 1208
QY 901 GTCTAGCGCGGCAAGCGCCCGCCCAAGAGGCGCTGACAGGCGAGCTGGCGCTGCTGTG 960
Db 1209 GTCTAGCGCGGCAAGCGCCCGCCCAAGAGGCGCTGACAGGCGAGCTGGCGCTGCTGTG 1268
QY 961 GACCCCAAGCGCGCGCTGTCCTTCAATCGCGCGCTTGGAGGACGAGAGGTGTGGAC 1020
Db 1269 GACCCCAAGCGCGCGCTGTCCTTCAATCGCGCGCTTGGAGGACGAGAGGTGTGGAC 1328
QY 1021 ATCATCTTGGCGCGCTGCGCCCAAGATCCCTGGCCACCCCAAGGTGACAGTTCGCTG 1080
Db 1329 ATCATCTTGGCGCGCTGCGCCCAAGATCCCTGGCCACCCCAAGGTGACAGTTCGCTG 1388
QY 1081 GTTACGCGCAAGCGCGCTTACGAGAGTGTGTAAGCGCATCGGACCAAGTACAGGCG 1140
Db 1389 GTTACGCGCAAGCGCGCTTACGAGAGTGTGTAAGCGCATCGGACCAAGTACAGGCG 1448

QY 1141 CGCGCAAGGCGTGGTCAAGTTCCTGGCGCCCTGGCGCACATGCTCACCGCGCGCC 1200
Db 1449 CGCGCAAGGCGTGGTCAAGTTCCTGGCGCCCTGGCGCACATGCTCACCGCGCGCC 1508
QY 1201 GACTTCATGCTGGTGGTCCCTCGCGCTTCGAGCCCTGAGCCCTGATCCAGCTGCACGCCATG 1260
Db 1509 GACTTCATGCTGGTGGTCCCTCGCGCTTCGAGCCCTGAGCCCTGATCCAGCTGCACGCCATG 1568
QY 1261 CACTACGCTACCGTCCCGTGGTACCTCCACCGCGCGCTGGTGCACACCGTC 1314
Db 1569 CACTACGCTACCGTCCCGTGGTACCTCCACCGCGCGCTGGTGCACACCGTC 1622

RESULT 7
AF433156 5856 bp DNA linear PLN 23-AUG-2002
LOCUS Chlamydomonas reinhardtii granule-bound starch synthase I (STA2)
DEFINITION gene, complete cds.
ACCESSION AF433156
VERSION AF433156.1 GI:16755882
KEYWORDS Chlamydomonas reinhardtii.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 5856) Chlamydomonas reinhardtii.
AUTHORS Wattbled,F., Buleon,A., Bouchet,B., Ral,J.P., Lienard,L.,
Delvalle,D., Bunderup,K., Dauvillee,D., Ball,S. and D'Hulst,C.
TITLE Granule-bound starch synthase I: a major enzyme involved in the
biogenesis of B-crystallites in starch granules
JOURNAL Eur. J. Biochem. 269 (15), 3810-3820 (2002)
PUBMED 12153578
REFERENCE 2 (bases 1 to 5856)
AUTHORS Wattbled,F., Ball,S.G. and D'Hulst,C.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2001) UMR8576 du CNRS, Laboratoire de Chimie
Biologique, Universite des Sciences et Technologies de Lille,
Villeneuve d'Ascq CEDEX 59655, France

FEATURES
Location/Qualifiers
1..5856
/organism="Chlamydomonas reinhardtii"
/db_xref="taxon:3055"
1343..>4911
/gene="STA2"
join(1343..1781,2151..2340,2484..2618,2815..2973,
3186..3373,3582..4117,4295..>4911)
/gene="STA2"
/product="granule-bound starch synthase I"
join(1480..1781,2151..2340,2484..2618,2815..2973,
3186..3373,3582..4117,4295..4911)
/gene="STA2"
/note="similar to the sequence deposited in GenBank
Accession Number AF026420; GBSSI"
/codon_start=1
/product="granule-bound starch synthase I"
/protein_id="AAL28128.1"
/db_xref="GI:16755883"
/translation="MAVASTSRPSARPVINAAGVYKKTANQLRLARGARKST
SRSAVTGATGATCALDIVNAAEVAPSWKSGTGLDVTGLPIEDYKRGHRVMTIAPRY
DQYADWTSVVVDIMGEKRYFHSIKKGVHVRWIDHPWFLAKVWKTGSKLYGPRSG
AYLDNHRFALFCKAIEAARVLFPFGEDCVFVANDWHSALVPLVKDEYQKGF
TKAGSVLAIHNIATFGWMEAFKDTKLPOAFDKLAFSDGVKVTYATATPMEDEKP
PLTGTYKKIINLKGSIITADKLIVTSYATATEIAADAGGVELTVIRAKGIEIVN
QMDIEWNPKTDFLSVPDQNSVYAGAAKEALQAEGLDVPDTPALFAPIGLEE
KMGDIILALPKILATPKVQIILGTGAAYEKLVNAIGTKYKRAKGVKFSAPLA
HMLTAGDFMLVPSRFEPGTLQHAMHYGVVAVSTGGLVDITKVGTFGHMGLN
FDKLDEADALATVRRASEVAGGRYPVMAVNTISODLSWSKPAQKWEGLLEVVY
KGGVYATAKEIKVPAEKIPGDLPAVSYPANTLKPVSASVEGNAAPKVGITAPA
MGAWRATPSGPSAAATPKVYTKPALPAITAKPTAGLKLAGEASTTSTSENGAAS
GNNGASASAKTSAAPLVSATPKSA"

BASE COUNT 1073 a 1816 c 1852 g 1115 t
ORIGIN

[illegible]


```

Db 842 CCACAGAGTTCAAGTCGCTTCATTCAGCGCTACGACAAG----- 888
QY 629 CCACCCCATGAGGAGGACGAGAGCCCGCTACGCGGAAGACCTACAGAAGATCA 688
Db 889 -----CCGCTGAGGGGGC-----AAGATCA 910
QY 689 ACTGGCTGAAGGGTGGCATTCATCGCGCCGACAAAGCTGGTGAAGTGTGCGCCAACTACG 748
Db 911 ACTGGATGAAGCGCGGATCTCGAGGCGGACAGAGGCTGACGGTGAGCCCTACTACG 970
QY 749 CGACCGAGATCGCTGCGCATCGCGCGCGGCTGTGGAGCTGGACACCGCTATCGCGCCA 808
Db 971 CTGAGGAGCTCATCTGCGGAAGCGAGGCTGCGAGCTCGACAACTATGCGCTCA 1030
QY 809 AGGCATTGAGGGATTGTGAACGCGATGGACATTGAGGATGGAAACCCAAAGCCGACA 868
Db 1031 CGGGATCACCGGATCTCAACGCGATGGACGTCAGTGAAGTGGAGCCCAAGGACA 1090
QY 869 AGTTCTGTCTGCGCCCTACGACAGAACAGCGTCTAGCGCGGCAAGCGCGCCCAAGG 928
Db 1091 AGTTCTCGCGCTCAACTACGACATACCACCGCTTGGAGGCCAAGCGCTGRACAAG 1150
QY 929 AGGCCCTGACGCGGAGTGGGCTGCTGTGGAGCCCGACCGCCCGCTGTTCGCTTCA 988
Db 1151 AGGCATGACGCGGAGTGGGCTGCGGTGAGTGAAGAGTGGCGTGTGCGCTTCA 1210
QY 989 TCGCGCCCTGGAGGAGCAGAAGGTTGTGGACATCATCTTGGCGCGCCCTGCCAAGATCC 1048
Db 1211 TCGCAGGCTGGAGGAGCAGAGGCGCGGACGTGATGTCGCGCCATCCCGGAGATCC 1270
QY 1049 TGGCCACCCCAAGTGCAGATCCCATCTCTGGTACCGGCAAGCGCGCTACGAGAAGC 1108
Db 1271 TGAAGGAGGAGGACGTCAGATCATCTCTTGGCACCGGGAAGAGTTGAGAAGC 1330
QY 1109 TGTGTAAGCGCATCGGACCAAGTACAGGCGCGCGCCAGAGGCGTGGTCAAGTTCTCG 1168
Db 1331 TGCTCAAGCATGAGGAGAGATTCCTCCGCGCAAGGTGAGGCGCGTGGTCAAGC 1390
QY 1169 CGCCCTGGCGGCATGCTACCGCGCGCGGCTTTCATGCTGGTGGCTCGCGCTTCG 1228
Db 1391 CGCGCTAGCTACCAAGATGATGCGCGCGCGGCTGCTGCTGCTCACCAGCGGCTTCG 1450
QY 1229 AGCCCTGGCGGCTGATCCAGCTCAGCGCATGACGATCGGTACGTCGCGCTGGTAGCCT 1288
Db 1451 AGCCCTGGCGGCTCATCAGCTCAGGGAATGCTATGGAACGCGGTGCGTGTGCGCT 1510
QY 1289 CCACGCGCGGCTGGTGCACACGCTC 1314
Db 1511 CCACGCGCGGCTCGTGCACACGATC 1536

RESULT 11
AF486518
LOCUS
DEFINITION
Hordeum vulgare cultivar SB 85750 mRNA linear PLN 02-JUL-2002
mRNA, complete cds.
ACCESSION
AF486518
VERSION
AF486518.1 GI:21667435
KEYWORDS
SOURCE
Hordeum vulgare.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 1827)
AUTHORS
Patron,N., Smith,A., Fahy,B., Hylton,C., Naidrett,M., Rossnagel,B.
and Denyer,K.
TITLE
A mutation in the 5' non-coding region of the barley GBS1 gene
alters its temporal and spatial expression and reduces GBS1
activity and amylose content in the endosperm
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1827)
AUTHORS
Patron,N.

```

```

Direct Submission
Submitted (22-FEB-2002) Metabolic Biology, John Innes Centre,
Norwich Science Park, Norwich, Norfolk NR4 7UH, UK
FEATURES
Location/Qualifiers
source
1..1827
/organism="Hordeum vulgare"
/cultivar="SB 85750"
/db_xref="taxon:4513"
1..1827
/codon_start=1
/product="granule bound starch synthase I"
/protein_id="AA074051.1"
/db_xref="GI:21667436"
/translation="MAALATLSOLATSGTGLVGTDRSAPMRHAGFCGLRPRKPADGT
FGMTVGASAPKPSRKRAHRCNCLSVVVRATSGMNLVFGAMFAWFKTGLGVDV
LGGLPAPAAAGHGVVVSRYDQYKDAWDSVISEIKVADEYERVFHCYKRGVDV
VFDHPHLEKVRGKTKETIYDQYDAGDIYEDNQQRFSLLQQAALAPRLNLRNPPYF
SGYGEDVFEVNDWHTGLLACYLKSNSYQNGIYRTAKVAFIHNIYQGELEISGEARG
QLNLDNRLKTSFDFIDGYDKPVEGRKINMKAGLQADKVLTVSPYAEELISGEARG
CELDNIMRLTGTIGVNGMDVSEWDPTKDFLAVNYDITALEAKALAKALQAEVL
PVRKVPVLAFAIGRLEBOKGPDVMIAPILPELKEEDVQIILIGTKKKPKLKSMEE
KFPKGVRAVRENAPLAHOMAGADLLAVTSREPCSLIQLOHRYGTTCVCASTGGL
VDRIYEGKTFNFMGRSLVDCNVVPEADVKAVITLKRKAVIKVGTPAYOEMVKNQMIOD
LSWKGPAKNWEDVILLEGVSGSEPFVIGVEIAPLAMEVNAAP"
BASE COUNT 364 a 567 c 602 g 294 t
ORIGIN
Query Match 34.8% Score 456.8; DB 8; Length 1827;
Best Local Similarity 62.2%; Pred. No. 1.8e-47;
Matches 837; Conservative 0; Mismatches 422; Indels 87; Gaps 4;
QY 5 TGGACATCGTGATGTTGCTGCTGAGTGGCGCTTGGTCCAAAGACGGCGGCTGGGCG 64
Db 242 TGAACCTCGTTCGTGCGCGCGAGATGGCGCTTGAGCAAGACCGCGGCTTGGCG 301
QY 65 ATGTGACTGTGGCTGCTGCTATTGAGTGTGTAAGCGCGGCCACCGCGTCAATGCTG 124
Db 302 ACGTCTCGCGCGGCTTCCACAGCCATGGCGCGCAACGGTCAAGGCTGATGCTGCT 361
QY 125 CCCCTCGTACGACAGTACGCTCAGCGCTGGGACCTCGTGGTGTGCTGACATCAGG 184
Db 362 CCCCGCGTACATCAGTACAGGACGCGCTGGACACAGCGCTCATCTCCAGATCAAG 421
QY 185 -----GGGGAAGTCCGCTACTTCCACTCATCAAGAAGGCGGTGACGCGC 232
Db 422 TCGTGACAGTACGAGAGGTGAGGTCTTCCACTGCTACAGCGGAGTGGACCGC 481
QY 233 TGTGATGACACCGCTGCTTCTGGCCAAAGTCTCGGGCAAGACCGGCTTCCAAAGTGT 292
Db 482 TGTTCATCGACACCGCTGCTTCTGGAGAAGGTCCGCGGCAAGACCAAGAGAATCT 541
QY 293 ACGGCGCGGCTCGCGGCTGACTACCTGGACACCAACAGCGCTTGGCTGTTCGCA 352
Db 542 ACGGCGCGGCTCGCGGCTGAGTACAGGACACCAAGCGCTTGGCTGTTCGCA 601
QY 353 AGGCGGCTATTGAGGCTGCGCGGCTGCTGCGCTTGGCGC----- 392
Db 602 AGGCGGCTCGAGGACCGCGGATCCTCAACCTCAACACACACCCCTACTTCTGCTC 661
QY 393 ----CGGCGAGGACTGGCTTCTGTCGCCAAAGCTGGGCTCGGCTGGTGGCGGCTC 448
Db 662 CCTACGGGAAGACGTGCTGCTGTCGAACACTGGCACACGCGGCTTCTGGCTGCT 721
QY 449 TGTGAAGGACGAGTACCGACCGCAAGGCGAGTTCACCAAGGCAAGTGGTGGCTGCT 508
Db 722 ACTCAAGACCACTACAGTCCCAAGCAATACAGGACCGGCAAGGTGGCTTCTGCA 781
QY 509 TCACAACTACGCTTCCAGGCGGCTGAGGAGGAGGCTTTCAAGGACACCAAGCTGC 568
Db 782 TCACAACTACGCTTCCAGGCGGCTTCTCTTCACGACTTGGCAGCTCAAGCTGC 841
QY 569 CCCAGGCGGCTTTGACAGCTGGCGCTTCTCGAGCGGCTATGCCAAGGTTTACACTGAG 628

```

```

842 CGACAGGTTCAAGTCGCTTCGACTTCATTGACGGCTACGACAAG----- 888
QY 629 CCACCCCCATGAGGAGGACGAGAGCCGCCCTGACGGGAAAGACCTACAGAAGATCA 688
Db 889 -----CCCGTGGAGGGCGC-----AAGATCA 910
QY 689 ACTGGCTGAAGGTGGCATTATCGCGCGGCGACAAGCTGTGACTGTGCGCCCACTAG 748
Db 911 ACTGGAAGGCGCGGATCTCTGCGAGCGGCGACAAGGTGCTGACGGTGAGCCCTACTAG 970
QY 749 CGACCCAGATCGTGCCTGCGGCTGCGCGGGGTGTGAGAGTGGACCCGCTCATCCGCCCA 808
Db 971 CTGAGAGCTCACTCTGCGGAAGCCAGGGGCTGCGAGCTCGACACATCATCGCGCTCA 1030
QY 809 AGGGCAITGAGGCGATGTGAAGCGCATGACATTCAGAGTGGAGACCCCAAGACCGACA 868
Db 1031 CGGGATACCGGGAATCGTCAACGGATGAGCGTCACTGAGTGGGACCCCAAGGACA 1090
QY 869 AGTTCGTGTCGCGCTACGACCAAGACAGCGTCTACGCGCGCAAGGCGCGCAAGG 928
Db 1091 AGTTCCTCGCGTCACTACGACATCACACCGCTTGGAGGCCAGGCGCTGAACAAGG 1150
QY 929 AGGCCCTGAGGCCGAGCTGGGCTGCTGTGGACCCCAAGCGCCCTGTCGCCCTTCA 988
Db 1151 AGGCACTGAGGCCGAGGTGGGCTGCGGTGGACAGGAAGTGGCGCTGGTGGCCTTCA 1210
QY 989 TCGGCCCTGAGGAGGACGAGGAGTGTGACATCATCTCGCGCGCCCTGCCCAAGATCC 1048
Db 1211 TCGGAGGCTGAGGAGGACGAGGCGCCGACGTGATGATCGCGCGCATCCCGGAGATCC 1270
QY 1049 TGGCCACCCCAAGGTGCAGATCGCATCTCGGTGACCGGCAAGGCGCGCTACGAGAAGC 1108
Db 1271 TGAAGGAGGAGCGTCCAGCATCTCTCTTGSCACCGGGAAGAAAGTTTGAGAAGC 1330
QY 1109 TGTGAAGCCCATCGGCACCAAGTACAAGGCGCGCGCAAGGCGGTGCTCAAGTTCGCG 1168
Db 1331 TGTCAAGAGCATGGAGGAGAGTTCCCGGGCAAGGTGAGGCGCGGTGTCAGGTTCAACG 1390
QY 1169 CGCCCTGGCGCATGCTCAACCGCGCGCGGCTTCTGCTGTCGCTCGCGCTCGGCTCG 1228
Db 1391 CGCGCTAGCTACAGATGATGCGCGCGCGGCTTCTGCTGCTGTCGCTGTCACGCGCTCG 1450
QY 1229 AGCCTCGGCGCTGATCCAGCTGCACGCCATGCACTACGTAACGTCGCCGCTGTAACCT 1288
Db 1451 AGCCTCGGCGCTCATCCAGCTCCAGGAAATGCGCTATGGAACCGCGCTGCGGTGCGGT 1510
QY 1289 CCACCGCGCGCTGCTGCGACCGTCTC 1314
Db 1511 CCACCGCGCGCTGCTGCGACCGATC 1536

RESULT 12
AF163319 LOCUS AF163319 2127 bp mRNA linear PLN 14-FEB-2000
DEFINITION Triticum aestivum granule-bound starch synthase I (Wx-D1) mRNA,
Wx-D1a allele, complete cds.
ACCESSION AF163319
VERSION AF163319.1 GI:6969977
KEYWORDS Triticum aestivum.
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 2127)
Vrinten, P.L. and Nakamura, T.
separate genes that are expressed in different tissues
Plant Physiol. 122 (1), 255-264 (2000)
JOURNAL 20098733
MEDLINE 10631269
PUBMED 10631269
REFERENCE 2 (bases 1 to 2127)

```

```

AUTHORS Vrinten, P.L. and Nakamura, T.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Crop Breeding, Tohoku National Agricultural
Experiment Station, Akihiro 4, Morioka, Iwate 020-0198, Japan
FEATURES
source Location/Qualifiers
1..2127
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/chromosome="7p"
/dev_stage="immature seed"
1..2127
/gene="Wx-D1"
/allele="Wx-D1a"
30..1844
/gene="Wx-D1"
/notes="Waxy protein; GBSSI"
/codon_start=1
/product="granule-bound starch synthase I"
/protein_id="AAF34135.1"
/db_xref="GI:6969978"
/translation="MAALVTSQATSGTVLGIITDRFRAGFGQVRPRSPADALGMRT
VGASAAPTOSRKAHRTTRCLSMVVRATSGGMNLFVGAEMAPYKSGKGLDVLGL
PRMAANGHRVWVISPRDYQKADWTSVVSSEIKVVDKYKRGVDRVFDV
HPCFLKVRGKKEKIYGPDACTDIEDNQRFSLCOAALEVPRIILNDDNPFESGPY
GEDVFVNDWHTGLLACYLKSNTQNGIIRAKVAFCTHNSIYQGRSFDDFAQLNL
PDRKSSFDIDYDKPVEGRKINMKAGILOADKVLTVSPYAEELISGEARGELD
NIMRLTGITGVNGMDVSEMDPTKRLAVNYDITALEGKALKNEALQAEVLVDR
KVLFAFICRLPEOKGPDVMAIAPELKEEDVQIVLGTGKKFKRLKSTEEKFPS
KYPAVRENAPLAHOMAGADVLAVTSRPEGLIOLQGMRYGTPCACAACSTGLVDTI
VEGKTFHMRGLSDCNVPEADVKVVTTLKRAVVGTPAYHVMVKNMIQDLWSK
GPAKNWEDVLELGVGSEFGEIAPLAMENVAAP"
BASE COUNT 452 a 617 c 687 g 371 t
ORIGIN
Query Match 34.8%; Score 456.8; DB 8; Length 2127;
Best Local Similarity 62.2%; Pred. No. 1.7e-47;
Matches 83; Conservative 0; Mismatches 422; Indels 87; Gaps 4;
QY 5 TGGACATCGTGATGGTGTCTGAGTTCGCCCTTGGTCCAAAGCGGGCGGCTCGGCG 64
Db 259 TGAACCTCGTGTCTGCGCGCGGAGATGGCGGCTGGAGCAAGACCGCGGCTCGGCG 318
QY 65 ATGTGACTGTGGGCTGCTTATTGAGCTGGTCAAGCGCGGCGGCTCATGACCATG 124
Db 319 ACGTCTCGGGGCGCTCCCGGCGGATGGCGGCGGCGGCGGCTCATGCTCT 378
QY 125 CCCCTCGCTACGACGATGACGCTGACGCTGGGACACCTCGGTGCTGTCGACATCATG 184
Db 379 CCCCGGCTAGCACCAGTACAAGGACGCGCTGGACACCGAGCTGCTCCGAGATCAAG 438
QY 185 -----GGGAGAAAGTCCGCTACTTCCACTCCATCCATCAAGAGGCGGTGACCGCG 232
Db 439 TCGTTGACAAGTACGAGAGGGTGAGTACTTCCACTGTACAAAGCGGGGTGACCGCG 498
QY 233 TGTGATGACACCCCTGTTCTTGGCCAAAGTCTGGGCAAGACCGGCTCCAAAGCTG 292
Db 499 TGTGCTCGACACCCCTGCTTCTTGGAGAGGCTCGGGGCAAGACCAAGAGAGATCT 558
QY 293 ACGGCCCGCTCGCGGCTGACTACCTGACCAACCAAGCGGTCCGCTGTCTGCA 352
Db 559 ACGGCCCGAGGAGCTGCTTCTGCGCAACAGCTGGCACTCCGCTGTGTCGCGCTCC 618
QY 353 AGGCGGCTATGAGGCTGCGCGGTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 388
Db 619 AGGCGGCTGAGAGTGGCGGAGATCCCTCAACCTCGACCAATAACCCCTACCTTTCTGGCG 678
QY 389 GCCCGCGGAGGAGCTGCTTCTGCGCAACAGCTGGCACTCCGCTGTGTCGCGCTCC 448
Db 679 CCTACGGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 738
QY 449 TGCTGAAGGAGGAGTACCAAGCGGCGGCTTCAACCAAGCGGAGCTGCTGCTGCTGCT 508

```


1

Db 320 ACGGGCGGACGCGCGGACGACTACGAGGACAACAGCAGCGCTTCAGCCTTCCTGTC 379
QY 353 AGCGCGCTATTGAGGCTGCCCGGCTGCTGCCCTTCG----- 388
Db 380 AGCGGCGCTGGAAGTGGCGGAGGATCGTAACCTGACAAATAACCCCTACTTTCTGGGC 439
QY 389 GCCCGCGGAGGACTGCGTTCGTGGCCAAACGACTGGCACTCGCCCTGGTGGCTTC 448
Db 440 CTTACGGGAGGAGCTGGTCTGCTGTGCAATGACTGGCACACGGGCTTCTGGCCTGCT 499
QY 449 TGTGTAAGGACGAGTACAGCCCAAGGCGGAGTTCACCAAGGCCAAGTGGTGGCTA 508
Db 500 ACTCAAGAGCAACTACCACTGCAATGGCATCTACAGGCGCGCAAGGTGGCACTGCA 559
QY 509 TCCACAACTCGCTTCAGGCGCGCATGTGGGAGGAGGCTTTCAGGACACGAAGTGC 568
Db 560 TCCACAACTCTGTAAGGCGCGCTTCTCTTCGACGACTTCGCGGAGCTCAACCTGC 619
QY 569 CCCAGGCGCCTTTGACAGCTGGCCTTCTCGGACGCTATGCAAGGTTTACACTGAGG 628
Db 620 CGACAGGTTCAAGTCTGCTTCGACTTTCATCGACGCTACGACAG----- 666
QY 629 CCACCCCATGAGGAGGAGGAGAGAGCCCGCGCTACGGGAAAGACCTACAGGAATCA 688
Db 667 -----CCGCTGAGGGGCGC-----AAGATCA 688
QY 689 ACTGGCTGAAGGCTGCAATTATCGCGCGGACAGCTGTGACTGTGTCGCCCACTAGC 748
Db 689 ACTGATGAGGCGCGGATTCCTGAGGCGGACAAAGTGTGCTGAGCTGAGCGCTTACG 748
QY 749 CGACCGAGATCTGCGGATCGCGCGGCTGTGAGCTGGACACCGTCATCCCGCA 808
Db 749 CGGAGGAGCTATCTCTGCGAAACAGGCGCTGAGCTGACAACTATCGGCTCA 808
QY 809 AGGGATTGAGGCGATTGTGAAGCGATGAGCAATTGAGGAGTGAACCCCAAGACGCA 868
Db 809 CTGGGATCACCGGCTGCTCAACGCGATGATGTTAGCGAGTGGGACCCCAAGGACA 868
QY 869 AGTCTCTGCTGCGCTTACGACGACAGACAGCTGTACCGCGGAGGCGCGCGCAAGG 928
Db 869 AGTCTCTGCGCTTAACTACGACATCAACCGCGCTTGGAGGGAAGGCGTGAACAAAG 928
QY 929 AGGCGCTGAGCGGAGCTGGCGCTTGTGGACCCCAAGCGCGCTGTTGCGCTTCA 988
Db 929 AGGCGCTGAGCGGAGCTGGCGCTTGTGGACCCCAAGCGCGCTGTTGCGCTTCA 988
QY 989 TCGCGCGCTGAGGAGGAGGAGTGTGACATCATCTGGCGCGCTGCCCCAAGATCC 1048
Db 989 TCGGAGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1048
QY 1049 TGGCACCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1108
Db 1049 TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1108
QY 1109 TGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1168
Db 1109 TACTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1168
QY 1169 CGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1228
Db 1169 CGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1228
QY 1229 AGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1288
Db 1229 AGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1288
QY 1289 CCACCGGCGGCTGGTGGACACCGCTC 1314
Db 1289 CCACCGGCGGCTGGTGGACACGATC 1314

RESULT 15

AF486519

LOCUS

DEFINITION

AF486519

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

DB 8;

Score

455.2;

Pred. No.

2.8e-47;

0;

423;

87;

286

124

346

184

406

232

466

292

526

Tue Jun 10 09:03:21 2003

Search completed: June 3, 2003, 13:34:27
Job time : 2303.88 secs

QY 293 ACGGCCCGCTCCGGCGTGTACTACTGACACACCAAGCGCTGCGCCTGTCTGTCCA 352
Db 527 ACGGCCCGGAGCGCGGACAGTATGAGACACACAGCGCTTCAGCCTTCTCTGCC 586
QY 353 AGCGCGCTATTAGGCTGCCGGTGTCTGCGCTTC-----G 388
Db 587 AGGACGACTCGAGGACCCAGGATCTCAACCTCAACAAACCCCTACTTTCTGTGC 646
QY 389 GCCCGCGGAGGACTGGCTTTCGTGGCCACAGCTCGGCTCGCCTGTGCGCGTCC 448
Db 647 CCTACGGGAGAGCGTGTCTTCGTGTGCAACAGCTGACACACGGGCTTCTGCGCTGT 706
QY 449 TGTGAAGGAGAGTACAGCCCAAGGCCAGTTCAACCAAGGCCAAAGTCGGTGTGGCTA 508
Db 707 ACCTCAAGAGCACTACAGTCCAAATGGCATCTACAGGACGGCCAAAGTGGCTTCTGCA 766
QY 509 TCCACAACATCCCTTCCAGGGCCGCAATGTGGAGAGGCTTTCAGGACACAGAGCTGC 568
Db 767 TCCACAACATCTCGTACCAGGGCGCTTCCTTCGACGACTTTGGCGAGCTCAACCTGC 826
QY 569 CCCAGGCGCGCTTTCACAAGCTGCGCTTCTCGGAGGCTATGCCAAGGTTTACACTGAGG 628
Db 827 CCGACAGGTTCAAGTCGTCTTCGACTTCAATGTCGGCTACGACAG-----873
QY 629 CCACCCCATGGAGGAGGACGAGAACGCCCGCTGACGGGAAGACCTACAGAAGATCA 688
Db 874 -----CCGCTGGAGGGCG-----AAGATCA 895
QY 689 ACTGCTGAAGGGTGGCAATTATPCGGCGCGGACAACTGGTGTGCTGCGCCCAACTAGG 748
Db 896 ACTGATGAAGSCGGGATCTGACAGCGCGGACAGAGTGTGACGGTGTGAGCCCTACTAGG 955
QY 749 CGACCGAGATCGCTCCCATGCGCGCGGGGTGGAGCTGACACACCGTCATCCGCGCA 808
Db 956 CTGAGGAGCTCATCTCTGGGAAGCAGGGGCTGCGAGCTGCAACATCATGCGGCTCA 1015
QY 809 AGGGCATTGAGGGCATTTGAACGGCATGGACATTTGAGAGTGGAAACCCCAAGACGACA 868
Db 1016 CGGGATCACCGAATGTCACAGGATGGAGCTCAGTGTGAGTGGGACCCCAAGGACA 1075
QY 869 AGTTCCTGTCTGCGCCCTACGACACAGAGCTGTACCGCGGCAAGCGCGCGCAAGG 928
Db 1076 AGTTCCTGCGCTCACTACGACATCACACCGCGCTTGGAGGCCAAGCGCTGAACAAGG 1135
QY 929 AGCCCTGACGCGGAGCTGGGCTGCTGTGAGCCCGCCCGCTGCTGCGCTTCA 988
Db 1136 AGGCGCTGACGCGGAGGTGGGCTGCGGCTGACAGGAGTGGCGCTGTGCGCTTCA 1195
QY 989 TCGGCGCGCTGAGGAGCAGAAGGCTGTGGACATCATCTGCGCGCCCTGCCCAAGATCC 1048
Db 1196 TCGGCGAGCTGAGGAGCAGAAGGCGCCGACGTGATGATCGCGCCATCCCGGAGATCC 1255
QY 1049 TGGCCACCCCAAGGTGCAAGTGCCTATCTGGGTACCGGACAGGCGCGCTACGAGAAGC 1108
Db 1256 TGAAGGAGGAGGAGCTCCAGATCATTTCTTGGCACCGGGAAGAGAAGTTTGAGAAGC 1315
QY 1109 TGGTGAACGCCATCGCACCAAGTACAAGGCGCGGCCCAAGGCGGTGGTCAAGTTCTCGG 1168
Db 1316 TGTCAAGAGCATGAGAGGAGAGTTCCCGGCAAGTGTGAGGCGCGTGTGAGGTTCAAGC 1375
QY 1169 CGCCCTGCGGCACATGCTCACCGCGCGCGGCGGCTTCAATGCTGTGCGCTGCGGCTCG 1228
Db 1376 CGCGGCTAGCTACCAAGATGATGGCGCGCGGCGGCTGTGCTGTGTCACCAAGCGCTTCG 1435
QY 1229 AGCCCTGCGGCGTGTACAGCTGCAAGCCATGCACTACGCTACCGTGGCGGTGAGCCT 1288
Db 1436 AGCCCTGCGGCGCTCATCCAGCTCCAGGAATGCGCTATGGAACGCGGTGCTGTGCGCGT 1495
QY 1289 CCACCGGCGGCTGGTGTGACACCGTC 1314
Db 1496 CCACCGGCGGCTGGTGTGACACGATC 1521

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 05:08:24 ; Search time 190.966 Seconds
(without alignments)
15495.523 Million cell updates/sec

Title: US-09-980-771A-6

Perfect score: 1314

Sequence: 1 gcgcgtgacatcgatggt.....gcgcctggtgcacaccgctc 1314

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002:*

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
- 2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
- 6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
- 7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
- 9: /SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
- 10: /SID52/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
- 11: /SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
- 12: /SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
- 13: /SID52/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
- 15: /SID52/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
- 16: /SID52/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
- 17: /SID52/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
- 18: /SID52/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
- 19: /SID52/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
- 20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400.6	30.5	2267	18 AAX63355	Granule bound star
2	387.4	30.2	1915	19 AAX60319	DNA sequence of th
3	388.4	29.6	2542	19 AAV29753	Oriza sativa waxy
4	281.8	21.4	2161	24 ABK53210	Potato granule-bou
5	271.2	20.6	2115	21 AAC32824	Arabidopsis thalia
6	217.2	16.5	2183	24 ABK53215	Canna edulis granu
7	203.8	15.5	2807	21 AAC86435	Wheat starch synth
8	203.8	15.5	2842	21 AAC86411	Wheat starch synth
9	202.6	15.4	2826	19 AAV01528	Wheat granule-bou

10	199.6	15.2	2380	19 AAV66834	zea mays soluble s
11	198.6	15.1	2478	18 AAT67287	Soluble starch syn
12	198.4	15.1	2107	21 AAC86412	Wheat starch synth
13	198.4	15.1	2107	21 AAC86431	Wheat starch synth
14	196.8	15.0	9024	21 AAC86431	Wheat SSII gene SE
15	193.6	14.7	2939	21 AAC86410	Wheat starch synth
16	193.6	14.7	2939	21 AAC86433	Wheat starch synth
17	193.2	14.7	2939	21 AAC86433	Wheat starch synth
18	193	14.7	2920	24 AAK88112	zea mays soluble s
19	191.4	14.6	2248	21 AAZ50651	CDNA encoding modi
20	191.4	14.6	2946	24 AAK88115	Corn starch synth
21	191.4	14.6	2951	24 AAK88114	CDNA encoding barl
22	191.2	14.6	2423	19 AAV70958	CDNA encoding barl
23	191	14.5	1798	21 AAZ50647	DNA encoding maize
24	191	14.5	2019	21 AAZ50646	Corn starch synth
25	191	14.5	2950	24 AAK88113	Corn starch synth
26	185	14.1	1724	24 ABR01821	CDNA encoding barl
27	151.2	11.5	2007	19 AAV70959	Rice starch synth
28	151.2	11.5	2007	19 AAV29754	DNA encoding maize
29	151.2	11.5	2085	18 AAT67286	zea mays soluble s
30	151.2	11.5	2085	19 AAV66833	Soluble starch syn
31	135.6	10.3	1479	24 ABQ90258	zea mays soluble s
32	135.6	10.3	1479	24 ABQ90406	M. capsulatus gene
33	125.6	9.6	333	21 AAC74569	M. capsulatus gene
34	125.6	9.6	333	24 ABN18316	Human OREF ORF124
35	116.8	8.9	2239	19 AAV01527	Human OREF polynuc
36	116.8	8.9	2805	21 AAZ24487	Wheat soluble star
37	114.6	8.7	2662	20 AAZ34651	Wheat soluble star
38	109.4	8.3	2533	15 AAQ45183	cDNA sequence of w
39	105.2	8.0	1984	21 AAC46797	Soluble rice starc
40	103.6	7.9	1758	17 AAT32325	Arabidopsis thalia
41	101.4	7.7	1528	21 AAZ50637	Soluble starch syn
42	101.4	7.7	1620	19 AAV29759	Corn soluble starc
43	101.4	7.7	1749	19 AAV70960	zea mays pEXS52 st
44	101.4	7.7	1752	19 AAV29756	DNA encoding maize
45	101.4	7.7	2008	21 AAZ50643	zea mays soluble s
					Corn soluble starc

ALIGNMENTS

RESULT 1
AAX63355
ID AAX63355 standard; cDNA; 2267 BP.
XX AAX63355;
AC AAX63355;
XX
XX
DT 16-JUL-1999 (first entry)
XX
DE Granule bound starch synthase encoding cDNA.
XX

Maize; corn; zea mays; delta-9 desaturase; GBSS; target; substrate;
granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
modulation; gene expression; transgenic plant; cleavage; canola plant;
caffeine synthesis; coffee plant; nicotine production; tobacco;
fruit ripening; flower pigmentation; lignin production; ss.
zea mays.
XX OS
XX WO9710328-A2.
PN
XX
PD 20-MAR-1997.
XX
XX 12-JUL-1996; 96WO-US11689.
XX
PR 13-JUL-1995; 95US-0001135.
XX
FA (DOWC) DOWELANCO.
FA (RIBO-) RIBOZYME PHARM INC.
XX
XX Edington BE, Folkerts O, Guo L, McSwiggen JA, Merlo DJ;
PI Merlo PAO, Skokut TA, Young SA, Zwick MG;

DR WPI: 1997-202224/18.
 XX Ribozyme which modulates plant gene expression - preferably
 PT modulates expression of DELTA-9 desaturase or granule bound starch
 PT synthase in maize or canola
 XX
 XX Example 9; Page 31-33; 155pp; English.
 XX
 CC The present invention describes an enzymatic nucleic acid molecule (I)
 CC with RNA cleaving activity, which modulates the expression of a plant
 CC gene. Also described is a gene comprising a cDNA sequence encoding maize
 CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
 CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
 CC gene, in a plant (preferably a maize or canola plant). (I) can be used
 CC to modulate caffeine synthesis in a coffee plant, nicotine production in
 CC a tobacco plant, fruit ripening processes in an apple, tomato, pear,
 CC plum or peach plant, flower pigmentation in a rose, petunia,
 CC chrysanthemum or marigold plant or lignin production in a tobacco,
 CC aspen, poplar or pine plant.
 XX
 SQ Sequence 2267 BP; 465 A; 699 C; 733 G; 370 T; 0 other;

Query Match 30.5%; Score 400.6; DB 18; Length 2267;
 Best Local Similarity 60.0%; Pred. No. 9.9e-59;
 Matches 810; Conservative 0; Mismatches 449; Indels 90; Gaps 5;

QY 5 TGGACATCGTGATGTTGCTGCTGAGTGGCGCCCTTGTGTCACAGAGCGGCGCCCTGGGCG 64
 DB 418 TGAACGTGCTGCTGCGGCCGAGATGGCCCGTGGAGCAAGACCGCGCCCTGGGCG 477
 QY 65 ATGTGACTGGTGGCTGCTATGTAGCTGGTCAAGCGGCGCCCGCTCATGACCATG 124
 DB 478 AGTCTCTGGCGGCGCTGCGCGGCATGGCGCGGAATGGGCACCGTGTATGTTGCTGT 537
 QY 125 CCCCTGCTACACACAGTACGCTGAGCGCTGGGACACCTCGTGGTCTGGGACAT----- 179
 DB 538 CTCCCGCTACGACAGTACAAAGAGCGCTGGGACACCAAGCGTGTCTCGAGATCAAGA 597
 QY 180 -----CATGGCGAGAGGTTCGGTACTTCCACTTCCATCAAGAGGCGGTGCACCGG 232
 DB 598 TGGAGACAGGTACGAGACGGTCAGGTCTTCCACTGTACAAAGCGCGAGTGGACCGG 657
 QY 233 TGTGATGTACACCCCTGGTTCCTGGGCAAGGCTGTGGGCAAGACCGGCTCCAGCTGT 292
 DB 658 TGTGCTTGCACCAACCCACTGTTCTCTGGAGAGGTTTGGGAAAGACCGAGGAGAAGATCT 717
 QY 293 AGGCGCCCGCTCGCGCTGACTACTGTGACCAACCAAGCGCTTCGCCCTGTTCTGCA 352
 DB 718 ACGGGCTCAGCGTGAACGGACTACAGGGAACCAACAGCTGCGGTTTCAGCCTGTATGC 777
 QY 353 AGGCGCTATTGAGGTGCGCGGTGCTGCGCTTCGCG----- 390
 DB 778 AGGACACTTGAAGCTTCAAGGATCTGAGCTCAACCAACCAACCACTTCTCGGAC 837
 QY 391 --CCGCGGAGAGCTGCTTCTGCGGCAAGCTGAGCTGGCACTCGGCCCTGGTCCCGTCC 448
 DB 838 CATACGGGAGGACGCTGCTGCTGCAAGCACTGGCACACCGGCCCTCTCTGCTGCT 897
 QY 449 TGTGAGGACGAGTACCAAGCCCAAGGCGAGTTACCAAGGCAAGTGGTCTGGCTA 508
 DB 898 ACCTCAAGAGCACTACCAAGTCCCGGCTTACAGGACGCAAGACCGCTTCTGCA 957
 QY 509 TCCACAACATCGCTTCCAGGCGCGCATGTGGAGGAGGCTTCAAGGACACGAAGCTGC 568
 DB 958 TCCACAACATCTCTACAGGCGCGGTTCGCCCTTCTCCGACTACCCGAGCTGAACCTCC 1017
 QY 569 CCAGGCGCGCTTGTACAGCTGGCTTCTCGGACCGGCTATGCCAAGGTTTACACTGAGG 628
 DB 1018 CGGAGAGATTCAAGTGTCTTCTGATTTCATCGACGGCTACGAGAAG----- 1064
 QY 629 CCACCCCGATGAGGAGGACGAGAACCGCCGCTGACGGGAAGACCTTCAAGAAGATCA 688
 DB 1065 -----CCCGTGGAG-----GCGGAGATCA 1086

QY 689 ACTGCTGAAGGGTGGCATTTATCGCGCGGCAAGCTGTGTGACTGTGTGCGCCACTAGG 748
 DB 1087 ACTGTATGAAGCGCGGATCTCTGAGGCGGACAGAGGTCTCTACCGTCAAGCCCTACTAGG 1146
 QY 749 CGACCGAGATCGTCCGATGCGCGGCGGTGTGAGCTGGACCGCTCATCCGCGCA 808
 DB 1147 CGAGGAGCTCATCTCCGGCATCGCCAGGGCTGCGAGCATCATGCGGCTCA 1206
 QY 809 AGGGCATTCAGGGCATTTGTAACGGCATGAGGAGTGAAGACCCCAAGACCGCA 868
 DB 1207 CCGGATCACCGGATCTCTACAGCATGAGCGTCAAGGAGTGGACCCCAAGGAGCA 1266
 QY 869 AGTTCCTGCTCGCGCTTACAGCAAGACAGCGTCTACCGCGCAAGGCGCGGCGCAAGG 928
 DB 1267 AGTACATCGCGTGAAGTACGACGCTGTCACGCGCGTGGAGGCCAAGGCGCTGAACAAGG 1326
 QY 929 AGGCCCTCAGCGCGAGCTGGGCTTCTGTCGACCCACCGCCCGCTTCTGCGCTTCA 988
 DB 1327 AGGCGCTGACGGCGGAGTTCGGGCTCCCGTGGACCGGAACATCCCGCTGTGGCGCTTCA 1386
 QY 989 TCGGCGCTCGAGGAGCAGAGGGTGTGGACATCATCTGCGCGCCCTGCCCAAGATCC 1048
 DB 1387 TCGGAGGCTGAAGAGCAGAGGACCGACGTCATGGGCGCGCATCCCGCAGCTCA 1446
 QY 1049 TGGCCACCCCAAG---GTGCAGATCGCCATCTCTGGTACCGGCAAGGCGCGCTACGAGA 1105
 DB 1447 TGGAGATGTTGAGGAGCGTGCATCTGCTGTGGCACCGGCAAGAGTTCGAGC 1506
 QY 1106 AGCTGTGTAACGCCATCGGCACCAAGTACAAGGCGCGCCCAAGGCGTGTCAAGTCT 1165
 DB 1507 GATGCTCATGAGCGCGGAGGAGGATTCAGAGGAGTGTCCGCGCGCGCTGGTCAAGTCA 1566
 QY 1166 CGGCGCCCTGGCGCACATGCTCACGCGCGCGCGGCACTTCACTGTGTGCTCGCGCT 1225
 DB 1567 ACGCGCGCTGGCGCACCATCATGTGCGCGCGCGGAGTGTCTCGCGCTCACCAGCGCT 1626
 QY 1226 TGAGCGCTTGGCGCTTCCAGCTGCACGCCATGCACTACGTAACGTCGCGCGTGTAG 1285
 DB 1627 TCGAGCGCTTGGCGCTTCCAGCTGCAGGGATGCGTACGAGCGCGCTGCGCGCTGCG 1686
 QY 1286 CTCCACCGCGCGCTGTCGACACCGTC 1314
 DB 1687 CGTCCACCGTGGACTGTCGACACCATC 1715

RESULT 2

AAX60319
 ID AAX60319 standard; DNA; 1915 BP.

XX AAX60319;

XX 23-AUG-1999 (first entry)

XX DNA sequence of the maize waxy gene.

XX Non-glycogen-like polysaccharide production; fermentation; waxy gene;
 KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;
 KW non-starch branching gene; amylopectin; amylose; plant-like starch; ss.

XX Zea mays.

XX WO9844780-A1.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-0506660.

XX 04-APR-1997; 97US-0042939.

XX (EXSE-) EXSEED GENETICS LLC.

XX Guan H, Keeling PL;